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SEQUENCE LISTING

(1) GENERAL INFORMATION:

5 (i) APPLICANT: (A) NAME: BRIGHAM AND WOMEN'S HOSPITAL (B) STREET: \$5 FRANCIS STREET (C) CITY: BOSTON (D) STATE: MASSACHUSETTS 10 (E) COUNTRY: USA (F) POSTAL CODE \((ZIP): 02115 (A) NAME: DANA-FÀRBER CANCER INSTITUTE (B) STREET: 44 BINNEY STREET (C) CITY: BOSTON 15

(D) STATE: MASSACHUSETTS

(E) COUNTRY: USA

(F) POSTAL CODE (ZIP): 02115

(ii) TITLE OF INVENTION: Novel Forms of T Cell Costimulatory Molecules and Uses Therefor

(iii) NUMBER OF SEQUENCES:

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: LAHIVE & COCKFIELD

(B) STREET: 60 State Street \ suite 510

(C) CITY: Boston

(D) STATE: Massachusetts

(E) COUNTRY: USA

(F) ZIP: 02109-1875

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk

(B) COMPUTER: IBM PC compatible

(C) OPERATING SYSTEM: PC-DOS/MS-DOS

(D) SOFTWARE: ASCII Text

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:

(B) FILING DATE:

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: US 08/205,697

(B) FILING DATE: 02-Mar-1994

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Mandragouras, Amy E.

(B) REGISTRATION NUMBER: 36,207

(C) REFERENCE/DOCKET NUMBER: BWI-120CPPC

(ix) TELECOMMUNICATION INFORMATION:

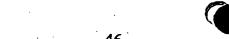
(A) TELEPHONE: (617)227-7400

(B) TELEFAX: (617)227-5941

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

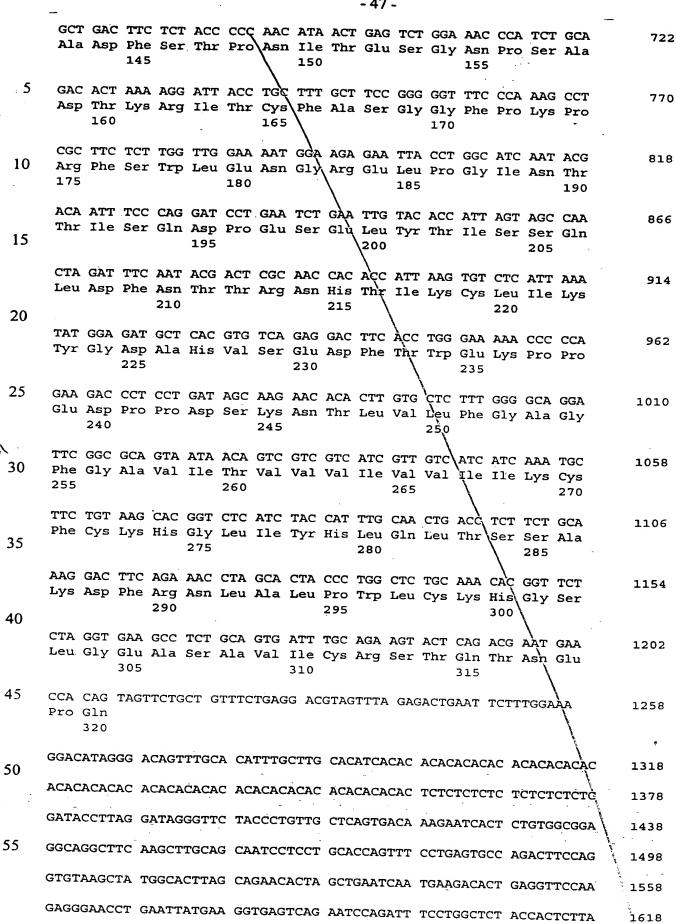
(A) LENGTH: 1888 base pairs



	j.	(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear
5	(ii)	MOLECULE TYPE: CDNA
	(ix)	FEATURE:
10		(A) NAME/KEY: CDS (B) LOCATION: 249. 1208
•	(xi)	SEQUENCE DESCRIPTION: SEQ
15	C 3 COOMMON A	· ·

ID NO:1:

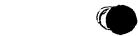
	(XI) SEQUENCE DESCRIPTION:\SEQ ID NO:1:														
15	GAGTTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACTCAA	CC 60													
	TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCG														
20	TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTTGT GAGCCTAGG														
	GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCCAAAGC														
25	CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu 1 5 10														
30	AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg 20 25 30	338													
, -	CTT TCA CAA GTG TCT TCA GAT GTT GAT GAA CAA CTG TCC AAG TCA GTG Leu Ser Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val	386													
35	AAA GAT AAG GTA TTG CTG CCT TGC CGT TAC AAC TCT CCT CAT GAA GAT Lys Asp Lys Val Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp 50 55 60	434													
40	GAG TCT GAA GAC CGA ATC TAC TGG CAA AAA CAT GAC AAA GTG GTG CTG Glu Ser Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu 65 70 75	482													
45	TCT GTC ATT GCT GGG AAA CTA AAA GTG TGG CCC GAG TAT AAG AAC CGG Ser Val Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg 80 85 90	530													
50	ACT TTA TAT GAC AAC ACT ACC TAC TCT CTT ATC ATC CTG GGC CTG GTC Thr Leu Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val 100 105 110	578													
	CTT TCA GAC CGG GGC ACA TAC AGC TGT GTC GTT CAA AAG AAG GAA AGA Leu Ser Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg	626													
55	GGA ACG TAT GAA GTT AAA CAC TTG GCT TTA GTA AAG TTG TCC ATC AAA Gly Thr Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser Ile Lys 130	674 ⁻													





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•	AC	CTGT	ATCT	GTT	AGAC	ccc :	AAGC'	rętg:	AG C	TCAT	AGAC	.: A AG	CTAA	TTTA	AAA	TGCT	TTT
5	TA	ATAA	GCAG	AAG	GCTC	AGT '	TAGT	ACGG	GG T	TCAG	GATA	C TG	CTTA	CTGG	CAA	TATT:	r ga
J	CT.	AGCC'	TCTA	TTT	rgtt:	rgt :	rttt"	/ AAAq	GG C	CTAC	TGAC	T GT	AGTG'	TAAT	TTG	TAGG	AAA
	CA'	TGTT	GCTA	TGT	ATAĊ	CCA :	rttg/	AGGG:	L' Y.	TAAA.	AATG'	r TG	GTAA'	TTTT	CAG	CCAGO	CAC
10	TT.	rcca(GGTA	TTT	CCT	TT 7	PATC	TTC	TT/								
	(2)) TNI	FORM	TT CN	I FOI				`	\			'				
15	(-)							NO:2		.\							
			(1)	(P) LE	NGTH	I: 32	0 am	ino		is \						
								line									
20		((ii)	MOLE	CULE	TYP	E: p	rote	in								
		((xi)	SEQU	ENCE	DES	CRIP	TION	: SE	Q II	, ио:	2:					
25	Met 1	Ala	Cys	Asn	Cys 5	Gln	Leu	Met	Gln	Asp 10		Pro	Leu	Leu	Lys 15	Phe	
\	Pro	Cys	Pro	Arg 20	Leu	Asn	Leu	Leu	Phe 25	Val	Leu	Leu	\Ile	Arg 30		Ser	
0	Gln	Val	Ser 35	Ser	Asp	Val	Asp	Glu 40	Gln	Leu	Ser	Lys	Ser 45	Val	.Lys	Asp	
5	Lys	Val 50	Leu	Leu	Pro	Cys	Arg 55	Tyr	Asn	Ser	Pro	His 60	Glu	Asp	Glu	Ser	
	Glu 65	Asp	Arg	Ile	Tyr	Trp 70	Gln	Lys	His	Asp	Lys 75	Val	Val	Leų	Ser	Val 80	
0	Ile	Ala	Gly	Lys	Leu 85	Lys	Val	Trp	Pro	Glu 90	Tyr	Lys	Asn	Arg	Thr 95	Leu	
	Tyr	Asp	Asn	Thr 100	Thr	Tyr	Ser	Leu	Ile 105	Ile	Leu	Gly	Leu	Val 110	Leu	Ser	
5	Asp	Arg	Gly 115	Thr	Tyr	Ser	Cys	Val 120	Val	Gln	Lys	Lys	Glu 125	Arg	Gly	Thr	
)	Tyr	Glu 130	Val	Lys	His	Leu	Ala 135	Leu	Val	Lys		Ser 140	Ile	Lys	Ala	Asp	
	Phe 145	Ser	Thr	Pro	Asn	Ile 150	Thr	Glu	Ser	Gly	Asn 155	Pro -	Ser	Ala	Asp	Thr 160	
5	Lys	Arg	Ile	Thr	Cys 165	Phe	Ala	.Ser	Gly	Gly 170	Phe	Pro	Lys	Pro	Arg 175	Phe	
	Ser	Trp	Leu	Glu 180	Asn	Gly	Ārģ	Glu	Leu 185	Pro	Gly	Ile	Asn	Thr 190	Thr	Ile	/

	Ser	Gln	Asp 195	Pro	Glu	ser	Glu	Leu 200	Tyr	Thr	:Ile	Ser	Ser 205	Gln	Leu	Asp		
5	Phe	Asn 210	Thr	Thr	Arg	Asn	His 215	Thr	Ile	Lys	Cys	Leu 220	Ile	Lys	Tyr	Gly	·	
	Asp 225	Ala	His	Val	Ser	Glu 230	Asp	Phe	Thr	Trp	Glu 235	Lys	Pro	Pro	Glu	Asp 240		
10	Pro	Pro	Asp	Ser	Lys 24 _. 5	Asn	Thr	Leu	Val	Leu 250	Phe	Gly	Ala	Gly	Phe 255	Gly		
15	Ala	Val	Ile	Thr 260	Val	Val	Val	Ile	Val 265	Val	Ile	Ile	Lys	Cys 270	Phe	Cys		
	Lys	His	Gly 275	Leu	Ile	Tyr	His	Leu 280	Gln	Leu	Thr	Ser	Ser 285	Ala	Lys	Asp		
20	Phe	A rg 290	Asn	Leu	Ala	Leu	Pro 295	Trp	Leu	Cys	Lys	His 300	Gly	Ser	Leu	Gly		
	Glu 305	Ala	Ser	Ala	Val	Ile 310	Cys	Arg	Ser	Thr	Gln 315	Thr	Asn	Glu	Pro	Gln 320		٠
25	(2)	INFC	RMAT	NOI	FOR	SEQ	ID N	10 : 3 :			'							
2 30		(i)	(A (E (C	l) LE 3) TY 1) SI	ENGTH PE: RAND	IARAC I: 25 nucl EDNE	16 b eic SS:	ase acid doub	pair I	·s			\					•
35		(ii)	MOL	ECUL	E TY	PE:	CDNA						\	\				
40			(B) NA) LC	ME/K CATI	EY: ON:	249.								\			
						SCRI						ጥ ሮ እ ሮ	<u>്</u> നന്	TC 3		CAACC		
45															/	CAACC CCGGG		60 120
	TGGA	TGCC.	AT C	CAGG	CTTC	т тт	TTCT	ACAT	CTC	TGTT	TCT (CGAT	TTTT	GT G	AGCC'	TAĢGA		180
50	GGTG	CCTA	AG C	TCCA	TTGG	C TC	TAGA	TTCC	TGG	CTTT	CCC (CATC	ATGT	rc T	CCAA	AGCĄT	•	240
55	CTGA	AGCT	ATG Met 1	Ala	TGC Cys	AAT Asn	TGT Cys 5	Gln	TTG Leu	ATG Met	CAG Gln	GAT Asp 10	ACA Thr	CCA Pro	CTC Leu	CTC Leu	\	290
	AAG 1 Lys 1	TTT (Phe :	CCA '	TGT Cys	CCA . Pro .	AGG (Arg 1	CTC . Leu .	AAT Asn	CTT (Leu :	Leu :	TTT (Phe '	GTG (CTG (Leu :	CTG /	AAT (Asn i	CGT Arg		338



	CT Le	TC u Se	A CAZ	GTC Val	TCT Ser	TCA Ser	GAT Asp	GT Val	T GA	T GA	u Gl	A CT	G TC	C AA r Ly	s Se	r Val	j L	386
5	AAI Lys	A GAT	r AAG D Lys	GTA Val	TTO	CTG Leu	CCT	TG(C CG' S Arg	r tac	C AAG	C TC:	r CC'	T CA' O Hi:	s Glu	_ 	Γ)	434
10	GAC Glu	TCI Ser	GAA Glu 65	Asp	CGA Arg	ATC	TAC	TGC Trp	o Gyi	A AAI 1 Lys	A CAT	GA(C AAI O Lys	3 Va	G GT(G CTO	;	482
15	TC1 Ser	GTC Val	ııe	GCT Ala	GGG Gly	AAA Lys	CTA Leu 85	AAA Lys	A GTG	TE	G CCC	GAG Glu	туз	AAC Lys	AAC Asr	C CGG	} ·	530
20	ACT Thr 95	Leu	TAT Tyr	GAC Asp	AAC Asn	ACT Thr 100	ACC Thr	TAC	TCI Ser	CTI Leu	Ile 105	: ATC	CTG Leu	GGC Gly	CTG Leu	GTC Val		578
	CTT Leu	TCA Ser	GAC Asp	CGG Arg	GGC Gly 115	ACA Thr	TAC Tyr	AGC Ser	TGT Cys	GTC Val 120	Val	ÇAA Gln	AAG Lys	AAG Lys	GAA Glu 125	AGA Arg		626
25	GGA Gly	ACG Thr	TAT Tyr	GAA Glu 130	GTT Val	AAA Lys	CAC His	TTG Leu	GCT Ala 135	TTA Leu	GTA Val	AAG Lys	TTG Leu	TCC Ser 140	Ile	AAA Lys		674
30	GCT Ala	GAC Asp	TTC Phe 145	TCT Ser	ACC Thr	CCC Pro	AAC Asn	ATA Ile 150	ACT Thr	GAG Glu	TCT Ser	GGA Gly	AAC Asn 155	CCA Pro	TCT Ser	GCA Ala		722
35	Asp	160	Lys	Arg	Ile		Cys 165	Phe	Ala	Ser	Gly	Gly 170	Phe	Pro	Lys	Pro		770
40	175	Pile .	ser	Trp	Leu	GAA Glu 180	Asn	Gly	Arg	Glu	Leu 185	Pro	Gly	Ile	Asn	Thr 190		818
4.5	1111	116	ser	GIN	Asp 195	Pro	Glu	Ser	Glu	Leu 200	Tyr	Thr	Ile	Ser	Ser 205	Gln\	١	866
45	Dea	Asp	Pne .	Asn 210	Tnr	ACT (Arg .	Asn	His 215	Thr	Ile	Lys	Cys	Leu 220	Ile	Lys		914
50	TYL	GIY.	Asp . 225	Ala .	H1S	GTG : Val :	ser (Glu 230	Asp	Phe :	Thr	Trp	Glu 235	Lys	Pro	Pro		962
55		240	PEO.	Pro A	Asp :	Ser I	Lys 1 245	Asn 	Thr	Leu	Val :	Leu 250	Phe	Gly	Ala	Gly		1010
	TTC Phe 255	GGC (GCA (Ala '	GTA A	rie .	ACA (Thr \ 260	STC (GTC (GTC . Val	Ile	GTT (Val ' 265	GTC . Val	ATC . Ile	ATC Ile	Lys	TGC Cys 270		1058

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5	TTC TGT AAG CAC AGA AGC TGT TTC AGA AGA AAT GAG GCA AGC AGA GAA Phe Cys Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu 275 280 285	1106
	ACA AAC AAC AGC CTT ACC TTC GGG CCT GAA GAA GCA TTA GCT GAA CAG Thr Asn Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln 290 300	1154
10	ACC GTC TTC CTT TAGTTCTTCT CTGTCCATGT GGGATACATG GTATTATGTG Thr Val Phe Leu 305	1206
15	GCTCATGAGG TACAATCTTT CTTTCAGCAC CGTGCTAGCT GATCTTTCGG ACAACTTGAC	1266
	ACAAGATAGA GTTAACTGGG AAGAGAAAGC CTTGAATGAG GATTTCTTTC CATCAGGAAG	1326
	CTACGGGCAA GTTTGCTGGG CCTTTGATTG CTTGATGACT GAAGTGGAAA GGCTGAGCCC	1386
20	ACTGTGGGTG GTGCTAGCCC TGGGCAGGGG CAGGTGACCC TGGGTGGTAT AAGAAAAAGA	1446
	GCTGTCACTA AAAGGAGAGG TGCCTAGTCT TACTGCAACT TGATATGTCA TGTTTGGTTG	1506
25	GTGTCTGTGG GAGGCCTGCC CTTTTCTGAA GAGAAGTGGT GGGAGAGTGG ATGGGGTGGG	1566
	GGCAGAGGAA AAGTGGGGGA GAGGGCCTGG GAGGAGGGA GGGAGGGGA CGGGGTGGGG	1626
	GTGGGGAAAA CTATGGTTGG GATGTAAAAA CGGATAATAA TATAAATATT AAATAAAAAG	1686
0	AGAGTATTGA GCGGTCTCAT CTACCATTTG CAACTGACCT CTTCTGCAAA GGACTTCAGA	1746
<u>, </u>	AACCTAGCAC TACCCTGGCT CTGCAAACAC GGTTCTCTAG GTGAAGCCTC TGCAGTGATT	1806
5	TGCAGAAGTA CTCAGACGAA TGAACCACAG TAGTTCTGCT GTTTCTGAGG ACGTAGTTTA	1866
	GAGACTGAAT TCTTTGGAAA GGACATAGGG ACAGTTTGCA CATTTGCTTG CACATCACAC	1926
^	ACACACACA ACACACACA ACACACACA ACACACACA	1986
0	TCTCTCTCTC TCTCTCTCT GATACCTTAG GATAGGGTTC TACCCTGTTG CTCAGTGACA	2046
	AAGAATCACT CTGTGGCGGA GGCAGGCTTC AAGCTTGCAG CAATCCTCCT GCACCAGTTT	2106
5	CCTGAGTGCC AGACTTCCAG GTGTAAGCTA TGGCACTTAG CAGAACACTA GCTGAATCAA	2166
	TGAAGACACT GAGGTTCCAA GAGGGAACCT GAATTATGAA GGTGAGTCAG AATCCAGATT	2226
`	TCCTGGCTCT ACCACTCTTA ACCTGTATCT GTTAGACCCC AAGCTCTGAG CTCATAGACA	2286
	AGCTAATTTA AAATGCTTTT TAATAAGCAG AAGGCTCAGT TAGTACGGGG TTCAGGATAC	2346
	TGCTTACTGG CAATATTTGA CTAGCCTCTA TTTTGTTTGT TTTTTAAAGG CCTACTGACT	2406
	GTAGTGTAAT TTGTAGGAAA CATGTTGCTA TGTATACCCA TTTGAGGGTA ATAAAAATGT	2466
٠	TGGTAATTTT CAGCCAGCAC TTTCCAGGTA TTTCCCTTTT TATCCTTCAT	2516

	(1) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 818 base pairs (B) TYPE: nucleic àcid	
5	(C) STRANDEDNESS: double	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
10		
10	(ix) FEATURE:	
	(A) NAME/KEY: CDS	
	(B) LOCATION: 1138	
15		-
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:	
	GGT CTC ATC TAC CAT TTG CAA CTG ACC TCT TCT GCA AAG GAC TTC AGA	
20	Gly Leu Ile Tyr His Leu Gln Leu Thr Ser Ser Ala Lys Asp Phe Arg	48
20	1 5 10 Asp Phe Arg	
	AAC CTA GCA CTA CCC TGG CTC TGC AAA CAC GGT TCT CTA GGT GAA GCC Asn Leu Ala Leu Pro Trp Leu Cys Lys His Gly Ser Leu Gly Glu Ala	96
25	20 25 Ser Leu Gly Glu Ala	
23	,	
	TCT GCA GTG ATT TGC AGA AGT ACT CAG ACG AAT GAA CCA CAG Ser Ala Val Ile Cys Arg Ser Thr Gln Thr Asn Glu Pro Gln	138
-	35 40 Pro Gln	
30		
	TAGTTCTGCT GTTTCTGAGG ACGTAGTTTA GAGACTGAAT TCTTTGGAAA GGACATAGGG	198
	ACAGTTTGCA CATTTGCTTG CACATCACAC ACACACACA ACACACACACACAC	258
2.5	ACACACACA ACACACACA ACACACACA TCTCTCTCT TCTCTCTC	230
35		318
	GATAGGGTTC TACCCTGTTG CTCAGTGACA AAGAATCACT CTGTGGCGGA GGCAGGCTTC	378
	AAGCTTGCAG CAATCCTCCT GCACCAGTTT CCTGAGTGCC AGACTTCCAG GTGTAAGCTA	
40		438
	TGGCACTTAG CAGAACACTA GCTGAATCAA TGAAGACACT GAGGTTCCAA GAGGGAACCT	498
	GAATTATGAA GGTGAGTCAG AATCCAGATT TCCTGGCTCT ACCACTCTTA ACCTGTATCT	
		558
45	GTTAGACCCC AAGCTCTGAG CTCATAGACA AGCTAATTTA AAATGCTTTT TAATAAGCAG	618
	AAGGCTCAGT TAGTACGGGG TTCAGGATAC TGCTTACTGG CAATATTTGA CTAGCCTCTA	
		678
	TTTTGTTTGT TTTTTAAAGG CCTACTGACT GTAGTGTAAT TTGTAGGAAA CATGTTGCŢA	738
50	TGTATACCCA TTTGAGGGTA ATAAAAATGT TGGTAATTTT CAGCCAGCAC TTTCCAGGTA	
	TTTCCCTTTT TATCCTTCAT	798
		818
55	(2)	-
, ,	(2) INFORMATION FOR SEO ID NO.5.	

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46 amino acids
- (B) TYPE: amino acid

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(D) TOPOLOGX: linear

(ii)	MOLECULE	TYPE:	proteir

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Gly Leu Ile Tyr His Leu Gln Led Thr Ser Ser Ala Lys Asp Phe Arg

1 10 15

Asn Leu Ala Leu Pro Trp Leu Cys Lys His Gly Ser Leu Gly Glu Ala 20 25 30

Ser Ala Val Ile Cys Arg Ser Thr Gln Thr Asn Glu Pro Gln
35 40 45

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1753 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- 25 (ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

GTTTTAGTAA CCAGAGGCCG CAAGAAGAGA TCACTTGTAT ATACACGGGC CCCATCTTTT 60 GCTTTTTAAG ACAAAAGAAA AAGAATCTTC TTCAACAAGT AAGTAAATGC ATTTACTATT 120 TATCATGCTA TGGGACACCT TAGTAGAACA CGCTATCTCC AGCCTTATCA TATGCATATT 180 TTGTTGTTGT TGTTGTTGTT GTTGTTAAAG ACAGGGTCTC ATATATGCCA GGCTGGTCCC 240 AAACTTTCAG TGTAACCCAA GATAATCTGG AACTCCCGAC TCCTCTGCTC CCACCTCTCC 300 AGTGCAGGAC ACTGTTTATA CCGTGCTGGG GAATTGAACT CAGAGCACCC TGCATGTCAG 360 CTAAGCATTC TACCGACCAA GTCCCATGCC CAGTCCCTAA CTCCCCAACT TCACTGCTTT 420 TTAAACATAC ATACAATCAT AACTTGCCCT CAGAGCAGTC TCCTGGGGTC TCTTATTCTC 480 AAGGCTGCGG CATTCCAACA CTGTTAGAAA AACACCATCA GGATTCTTTT $GTGTT_{\mathbb{C}}^{\mathbb{N}}$ CCTA 540 GATGCAAACA TTTTTGTAGG GCGAAGTTGA GGTTTTTCTA ATCAAGAAAA TGCCGGTAAC 600 AAGTCTCTTC AAGCTAACTG GTTGGCTAAG GGGTATCTCT CCAAAAGAAG AGATCCACAT 660 GTCAGGCCAG TTGTAGGCAT GATGTCAGGT CTCCCTCCCT TTCTTTCTTT CTTTCTTTT 720 780 GGTTTTTCGA GACAGGGTTT CTTTGTATAG CCCTGGCTGT CCTGGAACTC GCTCTGTAGA 840 CCAGGCTGGC CTCGAACTCA GAAATCTGCC TCTGCCTTTA CCTCCTGAGT GCTGGGAATT 900 AAAGGTGTGC ACCACCATGC CCGGCTGGGA TGTCATTCGT TTTCATTTCT CAATTTTGAT 960

40

45

55

ACTITATGGA AGAAAAAGA AAAGATAGAC AAGCCTCTTC ATGTAATACC CCATAGTCTC 1020 AATAAGTGGT GTTCGTAACG TGGCTTCTCT TTCCTTACCT TTTACTGGTA GATTTCTCGG 5 1080 TTGATTGATG TCCCTGTAGG ACTTACTGGG TTTAAGATTC TTGGTTTCCT GTTTTAAGAT 1140 ATAAAGAAAC CATTTCCTAA CTAAAACACT GCCTTGGACA AATATACTTT TGGCAGTCAC 1200 , 10 TCTGTGTCCA GAATGGAATT TAAGCTTTCA, TGGCCTAGCT GCTAGTGAAG GTTCTTTGCT 1260 TTTTTTTGGC TGTTGTATGT GAAATGGGGT TGGGTGGGAA CCACCTCACT GTGTTCTAGT 1320 GTTAGTCACC CCACCCCGC AAGCAGAATC CTTTTACCCA GCTTTTTCAC CCAGCTGTGC 15 1380 TCACCCGGTG CTCAGAACAG GCCTGGACAA GTCACCTCCC CTAGAGTTCT GGGGACCTTT 1440 GAGTTGCCCT CATGGCCACA CCCTGATTCA GAACTCTCAC TCTGTCGTAA GATAGAGCTA 1500 CTGGGGAGTT TTATACCTCA ATAGACTCTT ACTAGTTTCT CTTTTTCAGG TTGTGAAACT 20 1560 CAACCTTCAA AGACACTCTG TTCCATTTCT GTGGACTAAT, AGGATCATCT TTAGCATCTG 1620 CCGGGTGGAT GCCATCCAGG CTTCTTTTC TACATCTCTG TTTCTCGATT TTTGTGAGCC 1680 TAGGAGGTGC CTAAGCTCCA TTGGCTCTAG ATTCCTGGCT TTGCCCATCA TGTTCTCCAA 1740 AGCATCTGAA GCT 1753 30 (2) INFORMATION FOR SEQ ID NO:7: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 158 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: genomic DNA (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7: TGTCCAGGCA GAGCTAGTGG CTGCCCCTAG CGCTTCCTCT TCTTTGATAC CCCAAAGTCT 60 GAGTTTATTA CACATCCTTG GTGACCAAAT CACATGGGAG CTTCCTCCGA GGTCTTAGTA AAGGGAAGTT GGAAAGGGGA AATTCCTGCC CCCCTGCC 158 (2) INFORMATION FOR SEQ ID NO:8: (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1398 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA
- (ix) FEATURE:
 - (A) NAME/KEY: CDS

aporte de la compe

(B) LOCATION: 249..848

			•	(5)	LOCA	LION	: 24	98	48		•		_					
							/								•			
5		(x	i) S	EQUE	NCE I	DESCI	RIPT	ign:	SEQ	ID 1	NO : 8	:						
	GA	GTTT	TATA	CCT	CAATZ	AGA (CTCT	TACT	AG T	rrcr(CTTT	т тс	AGGT	TGTG	AAA	CTCAA	cc ·	60
	TT	CAAA	GACA	CTCT	rgti	CCA 1	TTC	rgtgo	GA C	TAAT	AGGA'	T CA	TCTT	TAGC	ATC:	rgccgo	≅G [`]	120
10	TG	GATG	CCAT	CCAC	GCTT	CT I	TTTC	CTAC	т Ç	CTG:	FTTC'	r cg	ATTT	TTGT	GAG	CCTAGG	BA	180
•						•	• .			./						AAAGCA		240
15	CT	SAAG	CT AT	rG GC et Al 1	T TO a Cy	SC AA 's As	T TO	T CA 's Gl 5	AG TI .n Le	rg Aq eu Me	rG CI	ln As	AT AG Sp Ti	CA CO	CA CT	CC CTC		290
20	AA(Lys	Phe	CCP Pro	TGT Cys	CCA Pro	AGG Arg 20	Leu	AAT Asn	CTI Leu	CTC Leu	TTO Phe	\.Val	G CTC	G CTO	3 ATT	CGT Arg		338
25	CT7 Lev	TCA Ser	CAA Gln	GTG Val	Ser 35	Ser	GCT Ala	GAC Asp	TTC Phe	TCT Ser 40	Thr	CCC Pro	AAC	ATA	A ACT Thr 45	GAG Glu		386
	TCI Ser	GGA Gly	AAC Asn	CCA Pro 50	Ser	GCA Ala	GAC Asp	ACT Thr	AAA Lys 55	Arg	ATT Ile	ACC Thr	TGC Cys	Phe	Ala	TCC Ser		434
<u>)</u>	GGG Gly	GGT Gly	TTC Phe 65	CCA Pro	AAG Lys	CCT Pro	CGC Arg	TTC Phe 70	TCT Ser	TGG Trp	TGG Trp	GAA Glu	AAT Asn 75	Gl _X	AGA Arg	GAA Glu		482
35	TTA Leu	Pro 80	GIY	ATC Ile	AAT Asn	ACG Thr	ACA Thr 85	ATT Ile	TCC Ser	CAG Gln	GAT A sp	CCT Pro 90	Glu	TCT	GAA Glu	TTG Leu		530
40	TAC Tyr 95	Inr	ATT	AGT Ser	AGC Ser	CAA Gln 100	CTA Leu	GAT Asp	TTC Phe	AAT Asn	ACG Thr 105	Thr	CGC Arg	AAC Asn	CAC His	ACC Thr 110		578
45	ATT Ile	AAG Lys	TGT Cys	CTC Leu	ATT Ile 115	AAA Lys	TAT Tyr	GGA Gly	GAT Asp	GCT Ala 120	CAC His	GTG Val	TCA Ser	GAG Glu	GAC Asp 125	TTC Phe	\	626
	ACC Thr	TGG Trp	GAA Glu	AAA Lys 130	CCC Pro	CCA Pro	GAA Glu	GAC Asp	CCT Pro 135	CCT Pro	GAT Asp	AGC Ser	AAG Lys	AAC Asn 140	ACA Thr	CTT Leu		674
50	GTG Val	CTC Leu	TTT Phe 145	GGG Gly	GCA Ala	GGA Gly	Phe	GGC Gly 150	GCA Ala	GTA Val	ATA Ile	ACA Thr	GTC Val 155	GTC Val	GTC Val	ATC Ile	- '	722
55	GTT Val	GTC Val 160	ATC Ile	ATC Ile	AAA Lys	TGC Cys	TTC Phe 165	TGT Cys	AAG Lys	CAC	AGA Arg	AGC Ser 170	TGT Cys	TTC Phe	AGA Arg	AGA Arg		770



-	AAT GAG GCA AGC AGA GAA ACA AAC AAC CTT ACC TTC GGG CCT GAA Asn Glu Ala Ser Arg Glu Thr Asn Asn Ser Leu Thr Phe Gly Pro Glu 175 180 185 190	818
5	GAA GCA TTA GCT GAA CAG ACC GTC TTC CTT TAGTTCTTCT CTGTCCATGT Glu Ala Leu Ala Glu Gln Thr Val Phe Leu 195 200	868
10	GGGATACATG GTATTATGTG GCTCATGAGG TACAATCTTT CTTTCAGCAC CGTGCTAGCT	928
	GATCTTTCGG ACAACTTGAC ACAAGATAGA GTTAACTGGG AAGAGAAAGC CTTGAATGAG	988
	GATTTCTTTC CATCAGGAAG CTACGGGCAA GTTTGCTGGG CCTTTGATTG CTTGATGACT	1048
15	GAAGTGGAAA GGCTGAGCCC ACTGTGGGTG GTGCTAGCCC TGGGCAGGGG CAGGTGACCC	1108
	TGGGTGGTAT AAGAAAAAGA GCTGTCACTA AAAGGAGAGG TGCCTAGTCT TACTGCAACT	1168
20	TGATATGTCA TGTTTGGTTG GTGTCTGTGG GAGGCCTGCC CTTTTCTGAA GAGAAGTGGT	1228
	GGGAGAGTGG ATGGGGTGGG GGCAGAGGAA AAGTGGGGGA GAGGGCCTGG GAGGAGAGA	1288
	GGGAGGGGGA CGGGTGGGG GTGGGGAAAA CTATGGTTGG GATGTAAAAA CGGATAATAA	1348
25	TATAAATATT AAATAAAAAG AGAGTATTGA GCAAAAAAAA AAAAAAAAAA	1398
	(2) INFORMATION FOR SEQ ID NO:9:	
30	(i) SEQUENCE CHARACTERISTICS:	•
ub_i	(A) LENGTH: 200 amino acids (B) TYPE: amino acid	
35	(D) TOPOLOGY: linear	
33	(ii) MOLECULE TYPE: protein	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:	
40	Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe 1 5 10 15	
	Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser	
45	Gln Val Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly 35 40 45	
50	Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly 50 55 60	· ·
30	Phe Pro Lys Pro Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro	-
	70 75 80	;
55	Gly Ile Asn Thr Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr 85 90 95	, v
	Ile Ser Ser Gln Leu Asp Phe Asn Thr Thr Arg Asn His Thr Ile Lys	į

Glu Lys Pro Pro Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu 130 Phe Gly Ala Gly Phe Gly Ala Val Ile Thr Val Val Val Ile Val Val 145 150 160 10 Ile Ile Lys Cys Phe Cys Lys His Arg Ser Cys Phe Arg Arg Asn Glu 165 180 180 180 180 180 180 180 18		Cys Leu Ile Lys Tyr Gly Asp Ala His Val Ser Glu Asp Phe Thr Trp 115 120 125
145 150 155 160 10 The lie Lys Cys Phe Cys Lys His arg Ser Cys Phe arg arg Asn Glu 175 Ala Ser Arg Glu Thr Asn Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala 180 180 185 190 Leu Ala Glu Gln Thr Val Phe Leu 195 200 (2) INFORMATION FOR SEQ ID NO:10: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1570 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: CDNA 30 (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 249890 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10: GAGTTITATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG ARACTCAACC TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTCCCGGG TGGATGCCATA CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTTGT GAGCCTAGGA GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCCAAAGCAT 45 CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu 1 10 AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu 11e Arg 15 20 20 20 20 30 CTT TCA CAA GTG TCT TCA GCT GAC TTC TCT ACC CCC AAC ATA ACT GAG Leu Ser Gln Val Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu 45 TCT GGA AAC CCA TCT GCA GAC ACT AAA AGG ATT ACC TGC TTT GCT TCC Ser Gly Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser	5	120
Ala Ser Arg Glu Thr Asn Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala 180 180 180 180 180 180 180 18		145
Leu Ala Glu Gln Thr Val Phe Leu 195 Leu Ala Glu Gln Thr Val Phe Leu 195 (2) INFORMATION FOR SEQ ID NO:10: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1570 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 249.890 (ix) SEQUENCE DESCRIPTION: SEQ ID NO:10: GAGGTITTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACTCAACC TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTTGT GAGCCTAGGA GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCC CATCATGTTC TCCAAAGCAT 45 CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu 1 5 10 AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg 15 20 CTT TCA CAA GTG TCT TCA GCT GAC TTC TCT TAC CCC AAC ATA ACT GAG Leu Ser Gln Val Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu 45 TCT GGA AAC CCA TCT GCA GAC ACT AAA AGG ATT ACC TGC TTC GCT Ser Gly Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser	10	1 <i>C</i> E • ===
(2) INFORMATION FOR SEQ ID NO:10: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1570 base pairs (B) TYPE: nucleic acid (C) STRANDENNESS: double (C) STRANDENNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: CDNA (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 249890 (Xi) SEQUENCE DESCRIPTION: SEQ ID NO:10: GAGGTTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACTCAACC TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG TGGATGCCAT CCAGGCTTCT TTTCTCTACAT CTCTGTTTCT CGATTTTTGT GAGCCTAAGCA 40 TGGATGCCAT CCAGGCTTCT TTTCTACAT CTCTGTTTCC CATCATGTTC TCCAAAGCAT 45 CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC Met Ala Cys Asn Cys Gin Leu Met Gin Asp Thr Pro Leu Leu 1 50 AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg 15 20 CTT TCA CAA GTG TCT TCA GCT GAC TTC TCT ACC CCC AAC ATA ACT GAG CTT TCA CAA GTG TCT TCA GCT GAC TTC TCT ACC CCC AAC ATA ACT GAG Leu Ser Gin Vals Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thr Giu TCT GGA AAC CCA TCT GCA GAC ACT AAA AGG ATT ACC TGC TTT GCT TCC Ser Gly Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser	15	100
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1570 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA (ii) MOLECULE TYPE: cDNA (iii) SEQUENCE DESCRIPTION: SEQ ID NO:10: GAGTTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACTCAACC TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTTGT GAGCCTAGGA GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCCAAACCAT 45 CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu 1		1
(A) LENGTH: 1570 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (C) STRANDEDNESS: double (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA 30 (ix) FEATURE: (B) LOCATION: 249.890 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10: GAGTTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACTCAACC TTCAAAGACA CTCTGTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTTGT GAGCCTAGGA GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCCAAAGCAT 45 CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu 1 50 AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg 15 CTT TCA CAA GTG TCT TCA GCT GAC TTC TCT ACC CCC AAC ATA ACT GAG Leu Ser Gln Val Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thir Glu 45 TCT GGA AAC CCA TCT GCA GAC ACT AAA AGG ATT ACC TGC TTT CCC 434 TCT GGA AAC CCA TCT GCA GAC ACT AAA AGG ATT ACC TGC TTT CCC 434 TCT GGA AAC CCA TCT GCA GAC ACT AAA AGG ATT ACC TGC TTT CCC 434 TCT GGA AAC CCA TCT GCA GAC ACT AAA AGG ATT ACC TGC TTT CCC 434 TCT GGA AAC CCA TCT GCA GAC ACT AAA AGG ATT ACC TGC TTT CCC 434	20	
(ii) MOLECULE TYPE: cDNA (ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 249890 (Xi) SEQUENCE DESCRIPTION: SEQ ID NO:10: GAGTTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACTCAACC TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTTGT GAGCCTAGGA GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCCAAAGCAT 45 CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu 1 5 10 AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg 15 20 25 30 CTT TCA CAA GTG TCT TCA GCT GAC TTC TCT ACC CCC AAC ATA ACT GAG Leu Ser Gln Val Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu 35 40 TCT GGA AAC CCA TCT GCA GAC ACT AAA AGG ATT ACC TGC TTT GCT TCC Ser Gly Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser	25	(A) LENGTH: 1570 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double
(A) NAME/KEY: CDS (B) LOCATION: 249.890 (Xi) SEQUENCE DESCRIPTION: SEQ ID NO:10: GAGTTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACTCAACC TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTTGT GAGCCTAGGA GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCCAAAGCAT 45 CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu 1 5 10 AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg 15 20 25 30 CTT TCA CAA GTG TCT TCA GCT GAC TTC TCT ACC CCC AAC ATA ACT GAG Leu Ser Gln Val Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu 45 TCT GGA AAC CCA TCT GCA GAC ACT AAA AGG ATT ACC TGC TTT GCT TCC Ser Gly Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser		
GAGTTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACTCAACC TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTTGT GAGCCTAGGA GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCCAAAGCAT 45 CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu 1 5 10 AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg 15 20 25 30 CTT TCA CAA GTG TCT TCA GCT GAC TTC TCT ACC CCC AAC ATA ACT GAG Leu Ser Gln Val Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu 45 TCT GGA AAC CCA TCT GCA GAC ACT AAA AGG ATT ACC TGC TTT GCT TCC 434 Ser Gly Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser	b.	(A) NAME/KEY: CDS
TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTTGT GAGCCTAGGA GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCCAAAGCAT 45 CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu 1 5 10 AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg 15 20 25 30 CTT TCA CAA GTG TCT TCA GCT GAC TTC TCT ACC CCC AAC ATA ACT GAG Leu Ser Gln Val Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu 45 TCT GGA AAC CCA TCT GCA GAC ACT AAA AGG ATT ACC TGC TTC CCC 434 Ser Gly Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser	35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:
TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTTGT GAGCCTAGGA GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCCAAAGCAT 45 CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu 1 5 10 AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg 15 20 25 30 CTT TCA CAA GTG TCT TCA GCT GAC TTC TCT ACC CCC AAC ATA ACT GAG Leu Ser Gln Val Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu 35 40 45 TCT GGA AAC CCA TCT GCA GAC ACT AAA AGG ATT ACC TGC TTT GCT TCC Ser Gly Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser		GAGTTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACTCAACC 6
GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCCAAAGCAT 45 CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu 1 5 10 AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg 15 20 25 30 CTT TCA CAA GTG TCT TCA GCT GAC TTC TCT ACC CCC AAC ATA ACT GAG Leu Ser Gln Val Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu 45 45 TCT GGA AAC CCA TCT GCA GAC ACT AAA AGG ATT ACC TGC TTT GCT TCC Ser Gly Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser	40	TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG 120
45 CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu 1 5 10 AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg 15 20 25 30 CTT TCA CAA GTG TCT TCA GCT GAC TTC TCT ACC CCC AAC ATA ACT GAG Leu Ser Gln Val Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu 35 40 45 TCT GGA AAC CCA TCT GCA GAC ACT AAA AGG ATT ACC TGC TTT GCT TCC Ser Gly Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser		TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTTGT GAGCCTAGGA 186
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Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg 20 25 30 CTT TCA CAA GTG TCT TCA GCT GAC TTC TCT ACC CCC AAC ATA ACT GAG Leu Ser Gln Val Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu 35 40 45 TCT GGA AAC CCA TCT GCA GAC ACT AAA AGG ATT ACC TGC TTT GCT TCC Ser Gly Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser	45	Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu
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Ser Gly Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser	55	Leu Ser Gln Val Ser Ser Ala Asp Phe Ser Thr Pro Asn Ile Thr Glu
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30	CAA	CTG	ACC	TCT	TCT	GCA	AAG	GAC	TTC	AGA	AAC	CTA	GCA	CTA,	CCC	таа	c	318
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2.5	CTC	TGC	AAA	CAC	GGT	TCT	CTA	GGT	GAA	GCC	TCT	GCA	GTG	TTA	TGC	AGA	8	166
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	TGAA	GAÇA	CT G	AGGT	TCCA	A GA	GGGA	ACCT	GAA	TTAT	GAA (GGTG	AGTC	AG A	ATCC	AGATT	12	80
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5 5	TCCT	(T)	_1 A(LCAC	TCTT	A AC	J'I'GT)	ATCT_	GTT.	AGAC	CCC 2	AAGC'	TČTG.	AG C	rcat:	AGACA	134	10
	AGCT	AATT:	TA A	ATG	CTTT:	TAI	AATA	GCAG	AAG	GCTC	AGT :	TAGT	ACGG	GG T	rcago	SATAC	14.0	00
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GTAGTGTAAT TTGTAGGAAA CATGTTGCTA TGTATACCCA TTTGAGGGTA ATAAAAATGT TGGTAATTTT CAGCCAGCAC TTTCCAGGTA TTTCCCTTTT TATCCTTCAT 5 (2) INFORMATION FOR SEQ ID NO:11: (i) SEQUENCE CHARACTER STICS: (A) LENGTH: 214 amino acids 10 (B) TYPE: amino adid (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11: Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe 1 20 Pro Cys Pro Arg Leu Ile Leu Leu Phe Val\Leu Leu Ile Arg Leu Ser Gln Val Ser Ser Ala Asp Phe Ser Thr Pro A igwedge Ile Thr Glu Ser Gly 25 Asn Pro Ser Ala Asp Thr Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly 50 Phe Pro Lys Pro Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro 30 Gly Ile Asn Thr Thr Ile Ser Gln Asp Pro Glu Ser Glu\Leu Tyr Thr Ile Ser Ser Gln Leu Asp Phe Asn Thr Thr Arg Asn His Thr Ile Lys 35 100 110 Cys Leu Ile Lys Tyr Gly Asp Ala His Val Ser Glu Asp Phe Thr Trp 120 40 Glu Lys Pro Pro Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val\Leu 135 Phe Gly Ala Gly Phe Gly Ala Val Ile Thr Val Val Val Ile Val 1 45

Ile Ile Lys Cys Phe Cys Lys His Gly Leu Ile Tyr His Leu Gln Leu 165 170 50 Thr Ser Ser Ala Lys Asp Phe Arg Asn Leu Ala Leu Pro Trp Leu Cys

180 185

Lys His Gly Ser Leu Gly Glu Ala Ser Ala Val Ile Cys Arg Ser Thr 200

Gln Thr Asn Glu Pro Gln 210

(2) INFORMATION FOR SEQ ID NO:12:

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				(A) N														
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		(XI) SE	QUEN	ICE D	ESCR	IPTI	ON:	SEQ	ID N	IO:12	2:						
	AGN	CCCN	AGA	TTAT	TTCT	cc c	TGTA	TAAG	G GA	rceco	CAGG	AGG	CCT	GGG	AGCG	GACAA	.G	60
20	GCT	CCTT	TTA	CTTT	TCTT	CT T	CTTC	TATI	T TI	TTTA	CGTI	CTA	TTTI	TTT	CTTC	ATGTT	'C	120
	CTG	TGAT	CTT	CGGG	AATG	CT G	CTGT	GCTT	G TG	TGTG	TGGT	CCC	TGAG	CGC	CGAG	GTGGA	.G	180
	AGG	CACT	GGT	GAC .	ATG	TAT	GTC	ATC	AAG	ACA	TGT	GC ₂	אככ	ፐርር	ACC	እጥሮ		220
25					Met	Tyr	Val	Ile	Lys	Thr	Cvs	Ala	Thr	Cvs	Thr	Met		229
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uDi																		
0	GGC	TTG	GCA	ATC	CTT	ATC	TTT	GTG	ACA	GTC	TTG	CTG	AŢC	TCA	GAT	GCT		277
30	Gly	Leu	Ala	Ile	Leu	Ile	Phe			Val	Leu	Leu	Ile	Ser	Asp	Ala		
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	CTT	TCC	GTG	GNG	N CC	C N N	COM	m » m	mma		~~~							
	Val	Ser	Val	GAG	Thr	CAA	VI a	TAT	Dho	AAT	GGG	ACT	GCA	TAT	CTG	CCG Pro		325
		30	• • • • • • • • • • • • • • • • • • • •	O L u		GIII	35	IYI	PHE	ASII	GIY	40	Ala	Тук	\ Leu	Pro		
35										•		40						
•	TGC	CCA	TTT	ACA	AAG	GCT	CAA	AAC	ATA	AGC	CTG	AGT	GAG	CTG	GTA	GTA		373
	Cys	Pro	Phe	Thr	Lys	Ala	Gln	Asn	Ile	Ser	Leu	Ser	Glu	Leu	Val	Val		3/3
	45					50					55				• • • • •	60		
40	_										,			•		\		
40	TTT	TGG	CAG	GAC	CAG	CAA	AAG	TTG	GTT	CTG	TAC	GAG	CAC	TAT	TTG	GĞ(C		421
	Pne	īrp	GIn	Asp	Gln	Gln	Lys	Leu	Val	Leu	Tyr	Glu	His	Tyr	Leu	Gl¾		
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45	Thr	Glu	Lvs	Leu	Asn	Ser	Val	AAI	Ala	AAG	TAC	CTG	GGC	CGC	ACG Thr	AGC		469
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	TTT	GAC	AGG	AAC	AAC	TGG	ACT	CTA	CGA	CTT	CAC	AAT	GTT	CAG	ATC	AAG	`	517
50	Phe	Asp	Arg	Asn	Asn	Trp	Thr	Leu	Arg	Leu	His	Asn	Val	Gln	Ile	Lvs		/21,
50			95					100		•		•	105					\
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	Den	ATG Mo+	GGC	TCG.	TAT	GAT	TGT	TTT	ATA-	CAA	AAA	AAG	CCA	CCC	ACA	GGA	•	565
	,πap	110	GIA	ser	ıyr'	Asp		Pne	тте	GIn	Lys		Pro	Pro	Thr	Gly	-	. /
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	Ser	Ile	Ile	Leu	Gln	Gln	Thr	Leu	Thr	Glu	Leu	Ser	Val	AIC	Ala	AAC		613
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	· · ·	TT(Phe	AGT Ser	GAA	CCI Pro	GAA Glu 145	Ile	AAA Lys	CTC	GCI Ala	CAG Gln 150	Asr	GTA Val	ACA Thr	GGA Gly	AAT Asn 155	TCT	. 66	61
•	5	GGC Gly	ATA Ile	AAT Asn	TTG Leu 160	Thr	TGC Cys	ACG Thr	TCT Ser	AAG Lys 165	Gln	GGI Gly	CAC His	CCG Pro	AAA Lys 170	Pro	' AAG Lys	70	09
	10	AAG Lys	ATG Met	TAT Tyr 175	Phe	CTG Leu	ATA Ile	ACT Thr	AAT Asn 180	Ser	ACT	AAT Asn	GAG Glu	TAT Tyr 185	Gly	GAT Asp	AAC Asn	75	57
	15	ATG Met	CAG Gln 190	ATA Ile	TCA Ser	CAA Gln	GAT Asp	AAT Asn 195	GTC Val	ACA Thr	GAA Glu	CTG	TTC Phe 200	AGT Ser	ATC Ile	TCC	AAC Asn	80)5
	20	AGC Ser 205	CTC Leu	TCT Ser	CTT Leu	TCA Ser	TTC Phe 210	CCG Pro	GAT Asp	GGT Gly	GTG Val	TGG Trp 215	CAT	ATG Met	ACC Thr	GTT Val	GTG Val 220	85	13
		TGT Cys	GTT Val	CTG Leu	GAA Glu	ACG Thr 225	GAG Glu	TCA Ser	ATG Met	AAG Lys	ATT Ile 230	TCC Ser	TCC Ser	AAA Lys	CCT Pro	CTC Leu 235	AAT Asn	90	1
N N N	25 ub l	TTC	ACT Thr	CAA Gln	GAG Glu 240	TTT Phe	CCA Pro	TCT Ser	CCT Pro	CAA Gln 245	ACG Thr	TAT Tyr	TGG Trp	AAG Lys	GAG Glu 250	ATT Ile	ACA Thr	94	9
	30	GCT Ala	TCA Ser	GTT Val 255	ACT Thr	GTG Val	GCC Ala	CTC Leu	CTC Leu 260	CTT Leu	GTG Val	ATG Met	CTG Leu	CTC Leu 265	ATC Ile	ATT Ile	GTA Val	99	7
	35	TGT Cys	CAC His 270	AAG Lys	ÀAG Lys	CCG Pro	AAT Asn	CÁG Gln 275	CCT Pro	AGC Ser	AGG Arg	CCC Pro	AGC Ser 280	AAC Asn	ACA Thr	GCC Ala	TCT Ser	104!	5
	40	AAG Lys 285	TTA Leu	GAG Glu	CGG Arg	GAT Asp	AGT Ser 290	AAC Asn	GCT Ala	GAC Asp	Arg	GAG Glu 295	ACT Thr	ATC Ile	AAC Asn	CTG Leu	AAG Lys 300	1093	3
		GAA Glu	CTT Leu	GAA Glu	CCC Pro	CAA Gln 305	ATT Ile	GCT Ala	Ser	GCA Ala	Lys	CCA Pro	AAT Asn	GCA Ala	GAG Glu			1,135	5

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TGAAGGCAGT GAGAGCCTGA GGAAAGAGTT AAAAATTGCT TTGCCTGAAA TAAGAAGTGC

AGAGTTTCTC AGAATTCAAA AATGTTCTCA GCTGATTGGA ATTCTACAGT TGAATAATTA

310

AAGAAC

125<u>5</u> 1261

1195

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 314 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13: Met Tyr Val Ile Lys Thr Cxs Ala Thr Cys Thr Met Gly Leu Ala Ile 5 5 10 : ` Leu Ile Phe Val Thr Val Leu Leu Ile Ser Asp Ala Val Ser Val Glu 25 Thr Gln Ala Tyr Phe Asn Gly Thr Ala Tyr Leu Pro Cys Pro Phe Thr 10 Lys Ala Gln Asn Ile Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp 50 55 15 Gln Gln Lys Leu Val Leu Tyr Glu His\Tyr Leu Gly Thr Glu Lys Leu **7**5 Asp Ser Val Asn Ala Lys Tyr Leu Gly Arg Thr Ser Phe Asp Arg Asn 20 Asn Trp Thr Leu Arg Leu His Asn Val Gln le Lys Asp Met Gly Ser 110 25 Tyr Asp Cys Phe Ile Gln Lys Lys Pro Pro Thr Gly Ser Ile Ile Leu 120 Gln Gln Thr Leu Thr Glu Leu Ser Val Ile Ala Asn Phe Ser Glu Pro 130 135 30 Glu Ile Lys Leu Ala Gln Asn Val Thr Gly Asn Ser Gly Ile Asn Leu 150 155 Thr Cys Thr Ser Lys Gln Gly His Pro Lys Pro Lys Lys Met Tyr Phe 35 Leu Ile Thr Asn Ser Thr Asn Glu Tyr Gly Asp Asn Met Gln Ile Ser 185 190 40

Gln Asp Asn Val Thr Glu Leu Phe Ser Ile Ser Asn Ser Leu\Ser Leu

200

Ser Phe Pro Asp Gly Val Trp His Met Thr Val Val Cys Val Leu Glu 215

Thr Glu Ser Met Lys Ile Ser Ser Lys Pro Leu Asn Phe Thr Gln Glu 230

Phe Pro Ser Pro Gln Thr Tyr Trp Lys Glu Ile Thr Ala Ser Val Thr 50 245 250

Val Ala Leu Leu Val Met Leu Leu Ile Ile Val Cys His Lys Lys 260 265

55 Pro Asn Gln Pro Ser Arg Pro Ser Asn Thr Ala Ser Lys Leu Glu Arg

Asp Ser Asn Ala Asp Arg Glu Thr Ile Asn Leu Lys Glu Leu Glu Pro 295 300

120

180

223

	<u> </u>
	Gln Ile Ala Ser Ala Lys Rro Asn Ala Glu
	305 310 \\
5	(2) INFORMATION FOR SEQ ID NO:14:
	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 223 base pairs
10	(B) TYPE: nucleic acid
io	(C) STRANDEDNESS: double
	(D) TOPOLOGY: linear \
	(ii) MOLECULE TYPE: cDNA
	(11) HOHECOBE TIPE: CDNA
15	
	(ix) FEATURE:
	(A) NAME/KEY: CDS
	(B) LOCATION: 194223
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20	\ =======
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:
	AGNCCCNAGA TTATTTCTCC CTCTATA AGG CAGGGGGGG
	AGNCCCNAGA TTATTTCTCC CTGTATAAGG GACGCCCAGG AGCCTGGGG AGCGGACAAG
25	GCTCCTTTTA CTTTCTTCT TCTTCTATTT TTTTTACCTT CTATTTTTT CTTCATGTTC
	· ·
	CTGTGATCTT CGGGAATGCT GCTGTGCTTG TGTGTGTGT CCCTGAGCGC CGAGGTGGAG
b	\
孙人	AGGCACTGGT GAC ATG TAT GTC ATC AAG ACA TGT GCA ACC TGC
	Met Tyr Val Ile Lys Thr Cys Ala Thr Cys
	1 5
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	(2) INFORMATION FOR SEQ ID NO:15:
35.	
	(i) SEQUENCE CHARACTERISTICS:
	(A) LENGTH: 10 amino acids
	(B) TYPE: amino acid
10	(D) TOPOLOGY: linear
ro	(ii) MOLEGUE E TUDE
	(ii) MOLECULE TYPE: protein
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:
_	/ 12 12 12 12 12 12 12 10 10:12:
-5	Met Tvr Val Ile Ive Thr Cve Ala Thr Cve

(2) INFORMATION FOR SEQ ID NO:16: 50 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1716 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 55

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS (B) LOCATION: 249..1166

5 (xi) SEQUENCE DESCRIPTION: SEO ID NO.16.

3		(xi	i) si	EQUEN	ICE D	ESCR	IPTI	ON:	SEQ	ID N	10:16	5:			•			
	GAG	TTT	ATA	CCTC	ATAA	GA C	TCTI	'ACTA	G TI	TCTC	TTT	TC	GGT	rgtg	AAAC	TCAA	CC .	60
10	TTC	'AAAC	ACA	CTCT	GTTC	CA T	ттст	GTGG	A CT	'AATA	GGAI	CAI	CTTT	ragc	ATCI	GCCG	G G	120
	TGG	ATGO	CAT	CCAG	GCTT	CT T	TTTC	TACA	тст	CTGI	TTCI	CGA	TTT	TGT	GAGO	CTAG	GA	180
	GGT	GCCI	'AAG	CTCC	ATTG	GC T	CTAG	АТТС	Ç TG	GCTT	TCCC	CAT	CATO	TTC	TCCA	AAGC	ΑT	240
15	CTG	AAGC	T AT Me	G GC	T TG a Cy	C AA	T TG	T CA	G TT	G AT u Me	G CA	G GA	T AC	A CC	A CT	C CTO	2	290
				1	_		_	5	\				0		O EC	u net	4	
20	AAG Lys 15	Phe	CCA Pro	TGT Cys	CCA Pro	AGG Arg 20	CTC Leu	AAT Asn	CTT Leu	Len	TTT Phe 25	Val	CTG Leu	CTG Leu	ATT	CGT Arg 30		338
25	CTT Leu	TCA Ser	CAA Gln	GTG Val	TCT Ser 35	TCA Ser	GAT Asp	GTT Val	GAT Asp	GAA Glu 40	CAA Gln	CTG	TCC Ser	AAG Lys	TCA Ser 45	GTG Val		386
30	AAA Lys	GAT Asp	AAG Lys	GTA Val 50	TTG Leu	CTG Leu	CCT Pro	TGC Cys	CGT Arg 55	TAC Tyr	AAC Asn	TCT Ser	CCT Pro	CAT His	GAA Glu	GAT Asp		434
bol.	GAG Glu	TCT Ser	GAA Glu 65	Asp	CGA Arg	ATC Ile	TAC Tyr	TGG Trp 70	CAA Gln	AAA Lys	CAT His	GAC Asp	AAA Lys 75	GTG Val	GTG Val	CTG Leu		482
35	TCT Ser	GTC Val 80	ATT Ile	GCT Ala	GGG Gly	AAA Lys	CTA Leu 85	AAA Lys	GTG Val	TGG Trp	CCC Pro	GAG Glu 90	TAT Tyr	AAG Lys	AAC Asn	CGG Arg		530
40	Thr 95	Leu	Tyr	Asp	Asn	ACT Thr 100	Thr	Tyr	Ser	Leu	Ile 105	Ile	Leu	Gly	Leu	Val 110		578
45	Leu	Ser	Asp	Arg	Gly 115	ACA Thr	Tyr	Ser	Cys	Val 120	Val	Gln	Lys	Lys	Glu 125	Arg		626
5.0	GGA Gly	ACG Thr	TAT Tyr	GAA Glu 130	GTT Val	AAA Lys	CAC His	TTG Leu	GCT Ala 135	TTA Leu	GTA Val	AAG Lys	TTG Leu	TCC Ser 140	ATC Ile	AAA Lys		674
	GCT Ala	GAC Asp	TTC Phe 145	TCT Ser	ACC Thr	CCC Pro	AAC Asn	ATA Ile 150	ACT Thr	GAG Glu	TCT Ser.	GGA Gly	AAC Asn 155	CCA Pro	TCT Ser	GCA Ala		722
55	GAC Asp	ACT Thr 160	AAA Lys	AGG Arg	ATT Ile	ACC Thr	TGC Cys 165	TTT Phe	GCT Ala	TCC Ser	GGG Gly	GGT Gly 170	TTC Phe	CCA Pro	AAG Lys	CCT Pro		770

	and the control of th	
	CGC TTC TCT TGG TTG GAA AAT GGA AGA GAA TTA CCT GGC ATC AAT ACG Arg Phe Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr 180 185 190	818
5	ACA ATT TCC CAG GAT CCT GAA TCT GAA TTG TAC ACC ATT AGT AGC CAA Thr Ile Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln 195 200 205	866
10	CTA GAT TTC AAT ACG ACT CGC AAC CAC ACC ATT AAG TGT CTC ATT AAA Leu Asp Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys 210 220	914
15	TAT GGA GAT GCT CAC GTG TCA GAG GAC TTC ACC TGG GAA AAA CCC CCA Tyr Gly Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro 225 230 235	962
20	GAA GAC CCT CCT GAT AGC AAG AAC ACA CTT GTG CTC TTT GGG GCA GGA Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly 240 245 250	1010
	TTC GGC GCA GTA ATA ACA GTC GTC GTC ATC GTT GTC ATC AAA TGC Phe Gly Ala Val Ile Thr Val Val Val Ile Val Ile Ile Lys Cys 255 260 265 270	1058
25	TTC TGT AAG CAC AGA AGC TGT TTC AGA AGA AAT GAG GCA AGC AGA GAA Phe Cys Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu 275 280 285	1106
30 D (ACA AAC AAC AGC CTT ACC TTC GGG CCT GAA GAA GCA TTA GCT GAA CAG Thr Asn Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln 290 295 300	1154
35	ACC GTC TTC CTT TAGTTCTTCT CTGTCCATGT GGGATACATG GTATTATGTG Thr Val Phe Leu 305	1206
	GCTCATGAGG TACAATCTTT CTTTCAGCAC CGTGCTAGCT GATCTTTCGG ACAACTTGAC	1266
40	ACAAGATAGA GTTAACTGGG AAGAGAAAGC CTTGAATGAG GATTTCTTTC CATCAGGAAG	1326
	CTACGGGCAA GTTTGCTGGG CCTTTGATTG CTTGATGACT GAAGTGGAAA GGCTGAGCCC	1386
	ACTGTGGGTG GTGCTAGCCC TGGGCAGGGG CAGGTGACCC TGGGTGGTAT AAGAAAAAAA	1446
45	GCTGTCACTA AAAGGAGAGG TGCCTAGTCT TACTGCAACT TGATATGTCA TGTTTGGTTG	1506
	GTGTCTGTGG GAGGCCTGCC CTTTTCTGAA GAGAAGTGGT GGGAGAGTGG ATGGGGTGGG	1566
50	GGCAGAGGAA AAGTGGGGGA GAGGGCCTGG GAGGAGAGGA	1626
	GTGGGGAAAA CTATGGTTGG GATGTAAAAA CGGATAATAA TATAAATATT AAATAAAAAG	1686
55	AGAGTATTGA GCAAAAAAA AAAAAAAAA	1716
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(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 306 amino acids

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(E) TYPE: amino acid (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe
1 5 10 15

Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser 20 25 30

Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp
35 40 45

Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser 50 55 60

20 Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu Ser Val 65 70 75 80

Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg Thr Leu
85 90 95

Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val Leu Ser

Asp Arg Gly Thr Tyr Ser Cys Val Val Gln Lys Lys Glu Arg Gly Thr
115 120 125

Tyr Glu Val Lys His Leu Ala Leu Val Lys Leu Ser \Ile Lys Ala Asp
130 135 140

35 Phe Ser Thr Pro Asn Ile Thr Glu Ser Gly Asn Pro Ser Ala Asp Thr 145 150 155 160

Lys Arg Ile Thr Cys Phe Ala Ser Gly Gly Phe Pro Lys Pro Arg Phe
165 170 175

Ser Trp Leu Glu Asn Gly Arg Glu Leu Pro Gly Ile Asn Thr Thr Ile
180 185 190

Ser Gln Asp Pro Glu Ser Glu Leu Tyr Thr Ile Ser Ser Gln Leu Asp

Phe Asn Thr Thr Arg Asn His Thr Ile Lys Cys Leu Ile Lys Tyr Gly 210 220

Asp Ala His Val Ser Glu Asp Phe Thr Trp Glu Lys Pro Pro Glu Asp 225 230 235 240

Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly Phe Gly
245 250 255

Ala Val Ile Thr Val Val Val Ile Val Val Ile Ile Lys Cys Phe Cys 260 265 270



Lys	His	Arg	Ser	CyĘ	Phe	Arg	Arg	Asn	Glu	Ala	Ser	Arg	Glu	Thr	Agn
		2/5		,	\		280	•	٠			285		•	
Asn	Ser 290	Leu	Thr	Phe	gly	Pro 295	Glu	Glu	Ala	Leu	Ala 300	Glu	Gln	Thr	Val

Phe Leu 305

- 10 (2) INFORMATION FOR SEQ ID NO:18:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1491 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

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- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 318..1181

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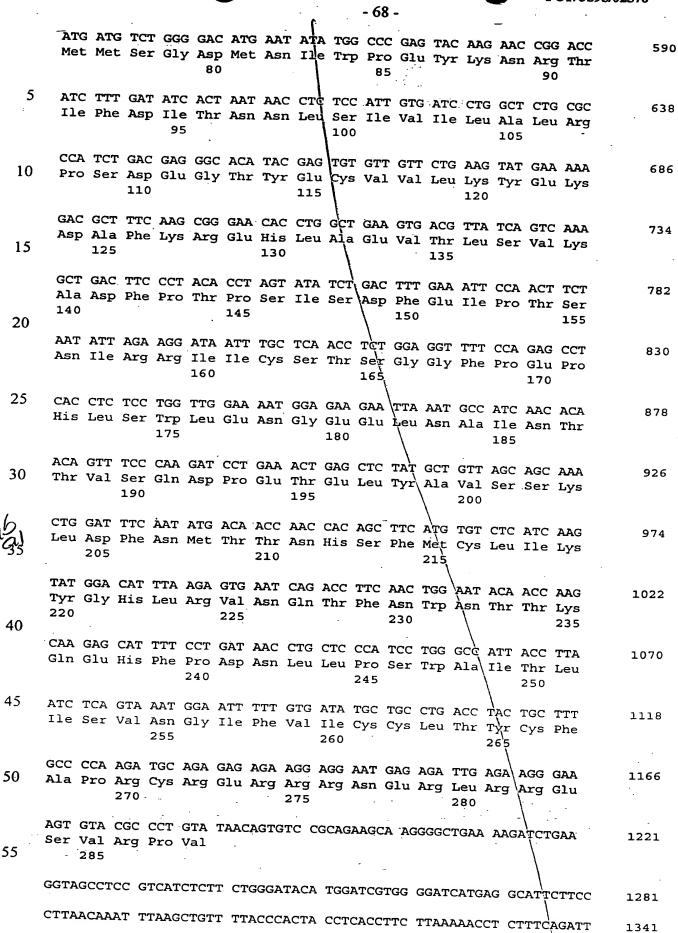
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CCA	AAGA	AAA	AGTG	ATTT	GT C	'ATTG	CTTI	TA TA	AGACT	GTA	GAZ	AGAGA	AACA	TCTC	CAGAAG	T	60
GGA	GTCT	TAC	CCTG	TAAA	CA A	AGGA	TTTA	A AG	AAAA	AGTG	GAZ	TTTT	TCT	TCAG	CAAGC	T	120
GTG	AAAC	TAA	ATCC	ACAA	.CC T	TTGG	AGAC	C CA	GGAA	CACC	CTC	raaj:	CTC	TGTG	TGTTT	т	180
GTA	AACA	TCA	CTGG	AGGG	TC T	TCTA	.CGTG	A GC	:AATT	GGAT	TĠI	CATC	AGC	CCTG	CCTGT	т	240
TTG	CACC	TGG	GAAG	TGCC	CT G	GTCT	TACT	T GG	GTCC	TAAA!	TGT	TGG	TTT	CACT	TTTGA(c	300
CCT.	AAGC.	ATC '	TGAA	GCC .	ATG (Met (GGC Gly	CAC . His	ACA Thr	CGG Arg 5	AGG Arg	CAG Gln	GGA Gly	ACA Thr	TCA Ser 10	CCA Pro		35 <u>0</u>
TCC Ser	AAG Lys	TGT Cys	CCA Pro 15	TAC Tyr	CTG Leu	AAT Asn	TTC Phe	TTT Phe 20	Gln	CTC Leu	TTG Leu	GTG Val	CTG Leu 25	Ala	GGT Gly		398
CTT Leu	TCT Ser	CAC His 30	TTC Phe	TGT Cys	TCA Ser	GGT Gly	GTT Val 35	ATC Ile	CAC His	GTG Val	ACC Thr	AAG Lys 40	GAA Glu	GTG Val	AAA Lys		446
GAA Glu	GTG Val 45	GCA Ala	ACG Thr	CTG Leu	TCC Ser	TGT Cys 50	GGT Gly	CAC His	AAT Asn	GTT Val	TCT Ser 55	GTT Val	GAA Glu	GAG Glu	CTG Leu	£ .	494
GCA Ala 60	GIII	ACT Thr	CGC Arg	ATC Ile	TAC Tyr 65	TGG Trp	CAA Gln	AAG Lys	GAG Glu	AAG Lys	AAA Lys	ATG Met	GTG Val	CTG Leu	ACT Thr	\	542

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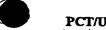


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AA	GCTG/	AACA	GTT	ACAA	TAE	GCTC	GCA?	rc c	CTCT	CCTT:	r CT	ccc	ATAT	GCA	ATTTG	CT
TAI	ATGT	AACC	TCT	CTTT	TTG d	CATO	TTT	CC A	TCTC	CCA	CT.	rgaa:	rtgt	CTT	STCAG	CC
AAT	TCAT	TAT	CTAT	TAAT 	ACA (TAAT	TTG	AG .							-	
(2)	INE	ORM	TION	, i FOF	SEC		t:01/	.9:					•			٠
		(i)	SEQU	JENCE	CHA	RACT	ERIS	TICS	S :							
			(2) LE	NGTH	l: 28 amin	8 an	ino		ls						
						GY:		•								
	(ii)	MOLE	CULE	TYP	E: p	rote	in\	\							
	(xi)	SEQU	ENCE	DES	CRIP	TION	: SE	Ø ID	NO:	19:					
Met 1	Gly	His	Thr	Arg 5	Arg	Gln	Gly	Thr	ser 10		Ser	Lys	Cys	Pro	Tyr	
Leu	Asn	Phe	Phe 20	Gln	Leu	Leu	Val	Leu 25	Ala	Gly	Leu	Ser	His 30	Phe	Cys	
Ser	Gly	Val 35	Ile	His	Val	Thr	Lys 40	Glu	Val	Lys	Glu	Val	Ala	Thr	Leu	
Ser	Cys 50	Gly	His	Asn	Val	Ser 55	Val	Glu	Glu	Leu	Ala	Gln	Thr	Arg	Ile	
Tyr 65	Trp	Gln	Lys	Glu	Lys 70	Lys	Met_	Val	Leu	Thr 75	Met	Met	Ser	Gly	Asp 80	
Met	Asn	Ile	Trp	Pro 85	Glu	Tyr	ГÀг	Asn	Arg 90	Thr	Ile	Phe	Asp	Ile 95	Thr	
Asn	Asn	Leu	Ser 100	Ile	Val	Ile	Leu	Ala 105	Leu	Arg	Pro	Ser	Asp	Glu \	Gly	
Thr	Tyr	Glu 115	Cys	Val	Val	Leu	Lys 120	Tyr	Glu	Lys	Asp	Ala 125		Lys	Arg	
Glu	His 130	Leu	Ala	Glu	Val	Thr 135	Leu	Ser	Val	Lys	Ala 140	Asp	Phe	Pro	Thr	
Pro 145	Ser	Ile	Ser	Asp	Phe 150	Glu	Ile	Pro	Thr	Ser 155	Asn	Ile	Arg	Arg	Ile 160	
Ile	Cys	Ser	Thr	Ser 165	Gly	Gly	Phe	Pro	Glu 170	Pro	His	Leu	Ser	Trp 175	Leu	12 T
Glu	Asn	Gly	Glu 180	Glu	Leu	Asn	Ala	Ile 185	Asn	Thr	Thr	Val	Ser 190	Gln	Asp	
Pro	Glu	Thr	Glu	Leu	Tyr	Ala 	Val	Ser	Ser	Lys	Leu	Asp	Phe	Asn	Met	\

	Th	r Thi 21(Asr	His	Se	r Phe	215	Cy i	s Lei	ı Ile	Lys	Tyr 220		y Hi	s Lei	u Arg	3	
5	Va:	l As r 5	ı Gln	Thr	Phe	230	Tri) Ası	n Thi	Thr	Lys 235		Glu	ı Hi	s Phe	Pro 240		
	Asj	o Asr	ı Leu	Leu	245	Ser	TT	Ala	a Ile	250		Ile	Ser	· Vai	l Asr 255	_	,	
10	Ile	e Phe	· Val	11e 260	Cys	Cys	Leu	Thi	Tyr 265		Phe	Ala	Pro	270		Arg	J -	
15	Glı	ı Arg	Arg 275	Arg	Asn	Glu	Arg	Let 280	Arg	Arg	Glu	Ser	Val 285		J Pro	Val		
	(2)	INF	'ORMA'	TION	FOR	SEQ	ID	NO : 2	0:	\								
20		(i	() ()	A) L: B) T C) S'	ENGT YPE : IRAN	HARA H: 1 nuc DEDN OGY:	151 leic ESS:	base aci dou	pai d	rs	\							
25		(ii) MOI	LECUI	LE T	YPE:	cDN.	A			\	-						•
Seph	1	(ix		4) NA	AME/	KEY:			_	•		\						
100	1		(1	3) L(JCAT.	ION:	99.	.102	5					,	,			
) W	1	(xi)					-			ID NO):20:		\	,				
35		GCAA) SEÇ GCA G	ÚENO GACGO	CE DI	ESCRI	IPTIC	ON: S	SEQ 1	AGGCA	GCA	CGGA	_ /				CT	. 60
35) SEÇ GCA G	ÚENO GACGO	CE DI	ESCRI	IPTIC	ON: S	SEQ 1	AGGCA	GCA	CGGA G GA	c c	C A	GA TO	3C	CT .	60
35	CCT	GCAA() SEÇ GCA G ACG T	QÚENC SACGO CGTTC	CE DI	ESCRI AG AG	PTIC	ON: (SEQ 1 I GTA	AGGCA CCAC	GCA G AT Me	CGGA G GA t As	C CC p Pr	CC A	GA TO	3C /s 5	CT .	
	CCT	GCAA) SEC GCA G ACG I GGC	QÚENC SACGO 'GTTO TTG	CE DI CGTAL CCAGA CCAGA	ESCRI AG AG AA CI ATC	PTICE CONTRACTOR CONTR	ON: S	SEQ 1 F GT# G CAC	AGGCA CCCAC	GCA G AT Me	CGGA G GA t As 1 GTC	C CC p Pr	CTG	GA TO	GC /s 5	CT	
	ACC Thr	GCAA(GTAG! ATG	SEQ GCA G ACG T GGC Gly	QÜENC GACGO TTTG Leu TCC	GCA Ala GTG	ESCRI AG AG AA CI ATC Ile	CTT Leu	ON: STOCK	SEQ I I GTA G CAC TTT Phe	AGGCA CCCAC GTG Val 15	GCA G AT Me ACA Thr	CGGA G GA t As: 1 GTC ' Val :	C CC p Pr TTG Leu	CTG Leu	GA TO	GC /s 5 TCA Ser	CT .	113
40	ACC Thr GAT Asp CTG Leu	GCAAC GTAGA ATG Met GCT Ala CCG Pro	GCA GACG TAGGET Val	TTG Leu TCC Ser 25	GCA Ala 10 GTG Val TTT Phe	AG AG ATC Ile GAG Glu	CTT Leu ACG Thr	ON: STOCK	SEQ I I GTA G CAC TTT Phe GCT Ala 30 CAA Gln	GTG Val 15 TAT Tyr	GCA G AT Me ACA Thr TTC	CGGA G GA t As: 1 GTC ' Val : AAT (Asn (AGC (Ger I	C CC p Pr TTG Leu GGG Gly CTG Leu 50	CTG Leu ACT Thr 35 AGT Ser	ATC Ile 20 GCA Ala GAG Glu	TCA Ser TAT Tyr	CT	161
40 45	ACC Thr GAT Asp CTG Leu	GCAAC GTAGA ATG Met GCT Ala	GCA GACG TAGGET Val	TTG Leu TCC Ser 25 CCA Pro	GCA Ala 10 GTG Val TTT Phe	AG AG ATC Ile GAG Glu ACA Thr	CTT Leu ACG Thr AAG Lys	ON: STOCK	SEQ I I GTA G CAC TTT Phe GCT Ala 30 CAA Gln	GTG Val 15 TAT Tyr	GCA GAT Me ACA Thr TTC Phe ATA Ile	CGGA G GA t As: 1 GTC ' Val : AAT (ASn (Ser I	C CC p Pr TTG Leu GGG Gly CTG Leu 50	CTG Leu ACT Thr 35 AGT Ser	ATC Ile 20 GCA Ala GAG Glu	TCA Ser TAT Tyr	CT	113 161 209

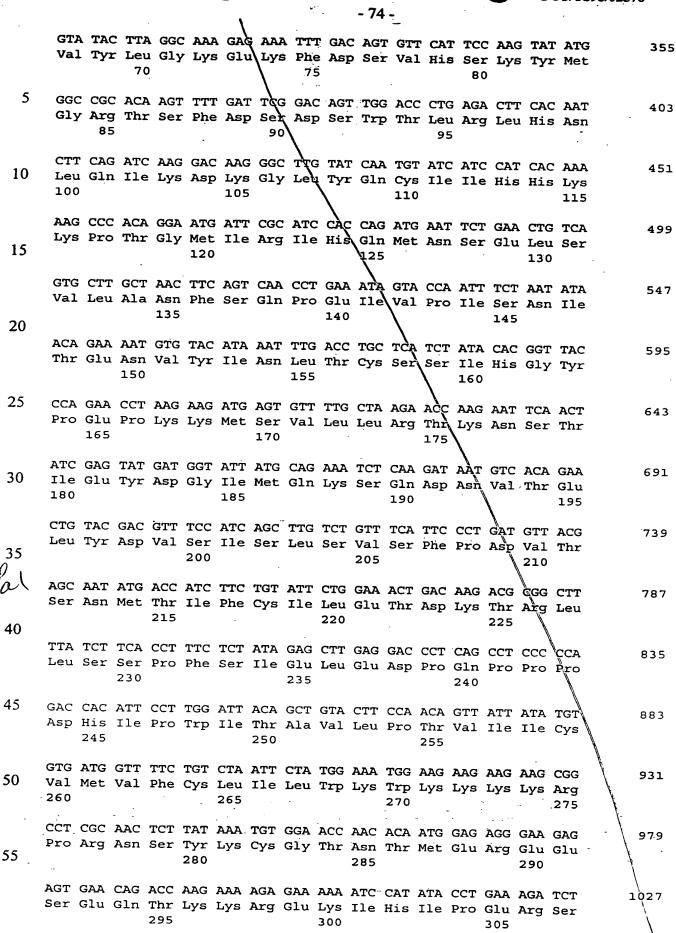


							. 2,		٠	:								
	ACC Thr	AGC Ser	TTT Phe	GAC Asp	AGG Arg	AAC Asq	AAC	TGG	ACT	CTA	Arg	CTI Leu	CAC His	AAT Asn	Val	CAG Gln	401	
5							\ .	•		95	•				100			
	ATC	AAG	GAC	ATG	GGC	TCG	TĄT	GAT	TGT	TTT	ATA	CAA	AAA	AAG	CCA	CCC	449	
	Ile	Lys	Asp	Met	Gly	Ser	Tyk	Asp	Cys	Phe	Ile	Gln	Lys	Lys	Pro	Pró	• • • •	
				105			. /	\	110					115			•	
10	ארא	CCA	ጥርክ	א מוומי	אשר	OTTO	<i>-</i>	/~~		-								
10	Thr	GGA Gly	Ser	Tle	Tle	Leu	Gln	Gin	Thr	Leu	ACA Th∽	GAA	CTG	TCA	GTG	ATC	497	
		-4	120					125		Lea	. 1111	GIU	130		vai	116		
							• .	- /										
15	GCC	AAC	TTC	AGT	GAA	- CCT	GAA	ATA	AAA	CTG	GCT	CAG	AAT	GTA	ACA	GGA	545	
15	Ala	Asn 135	Pne	Ser	Glu	Pro		Ile	\Lys	Leu	Ala		Asn	Val	Thr	Gly		
		133					140		\			145						
	AAT	TCT	GGC	ATA	AAT	TTG	ACC	TGC	ACG	TCT	AAG	CAA	GGT	CAC	CCG	272	593	
20	Asn	Ser	Gly	Ile	Asn	Leu	Thr	Cys	Thr	Ser	Lys	Gln	Gly	His	Pro	Lys	393	
20	.150					155			\		160		_			165		
	CCT	አክሮ	7 7 C	אתרי	m s m	mmm	ama			\ \								
	Pro	AAG Lys	Lvs	Met	Tvr	Phe	Len	TIA	ACT	AAT	TCA	ACT	AAT	GAG	TAT	GGT	641	
		-1-	-1-		170			110	1111	175	ser	III	ASII	GIU	1yr 180	GIY		
25																		
	GAT	AAC	ATG	CAG	ATA	TCA	CAA	GAT	AAT	GTC	\ACA	GAA	CTG	TTC	AGT	ATC	689	
	Asp	Asn	Met		Ile	Ser	Gln	Asp.		Val	Thr	Glu	Leu	Phe	Ser	Ile		
				185					190					195				
30	TCC	AAC	AGC	CTC	TCT	CTT	TCA	TTC	CCG	GAT	GGT	GTG	TGG	СУТ	ልጥር	አሮር	737	
	Ser	Asn	Ser	Leu	Ser	Leu	Ser	Phe	Pro	Asp	Gly	\val	Trp	His	Met	Thr	737	
			200			-		205				\	210					
	CTT	CTC	mam.	CMM	C TO C	<i>~</i>												
35	Val	GTG Val	Cvs	Val	Leu	GAA	Thr	GAG	TCA	ATG	AAG	ATT	TCC	TCC	AAA	CCT	785	
<u>L</u>		215	-1-	,			220	GIU	Ser	MEC	цур	225	Ser	ser	ьуs	Pro		
\mathcal{U}_{λ}													\					
\mathcal{U}'	CTC	AAT	TTC	ACT	CAA	GAG	TTT	CCA	TCT	CCT	CAA	ACG	TAT	TGG	AAG	GAG	833	
40	230	Asn	Phe	Thr	Gln		Phe	Pro	Ser	Pro		Thr	TYT	\mathtt{Trp}	Lys	Glu		-
	230					235				-	240		\			245		
	ATT	ACA	GCT	TCA	GTT	ACT	GTG	GCC	CTC	CTC	CTT	GTG	ATG	GTG	CTC	እጥ <u></u> ር	881	
	Ile	Thr	Ala	Şer	Val	Thr	Val	Ala	Leu	Leu	Leu	Val	Met	Leu	Leu	Ile	991	
45					250					255				\	260			
43	דידע	GTA	ጥር።	CNC	ת ת	N N C	CCC	7. 7. CT	G 7 G	aam.				\				
	Ile	GTA Val	Cvs	His	Lvs	Lvs	Pro	Asn	Gln	Pro	AGC	AGG	CCC	AGC V	AAC	ACA	929	
			-1-	265	-7-	_,.		71011	270	110	Ser	Arg	PIO	275	Asn	Thr		
50									-						\			
50	GCC	TCT	AAG	TTA -	GAG	CGG	GAT	AGT	AAC	GCT	GAC	AGA	GAG	ACT .	АТС.	AAC	977	
•	Ala	Ser	Lys 28Ö	Leu	Glu	Arg	Asp -		Asn	Ala	Asp			Thr	Ile\.	Àsn		
			200					285			*		290		· /			
	CTG	AAG	GAA	CTT	GAA	CCC	CAA	ATT	GCT	TCA	GCA	AAA	CCA	Д ДΨ	GC Þ	GDG /	1025	
55	Leu	Lys	Glu	Leu	Glu	Pro	Gln	Ile	Ala	Ser	Ala	Lys	Pro	Asn	Ala	Glu	1025	
		295					300					305			-	\		
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		.JUCA		AGAG		שט אי	AAAG	MGTT	AAA	AATT	GCT	TTGC	CTGA	AA T.	AAGA.	AGTGC	1085	



	AGA	GTTI	CTC	AGAA	TTCA	ÀA A	ATGI	TCTC	A GO	TGAT	TGGA	L ATT	CTAC	AGT	TGAA	ATTAATTA
	AAG	AAC							\							
5									\							
	(2)	INF	ORMA	TION	FOR	SEQ	ID	NO : 2	:1:\							
		-	(i)	SEQU												
10				(B			amin		ino \ id	acid	s					
				(D) ŢO	POLO	GY:	line	ar	\						
		(ii)	MOLE	CULE	TYP	E: p	rote	in							
15		. (xi)	SEQU	ENCE	DES	CRIP	TION	: SE	σip	NO:	21:				<u>.</u> *
	Met 1		Pro	Arg	Cys 5	Thr	Met	Gly	Leu	Ala		Leu	Ile	Phe		Thr
20	**- 3	•	•	_,		_	_ •				\			•	15	
20	VaI	Leu	Leu	Ile 20	Ser	Asp	Ala	Val	Ser 25	Val	.G1\u	Thr	Gln	Ala 30	_	Phe
	Asn	Gly	Thr	Ala	Tyr	Leu	Pro		Pro	Phe	Thr	f\ than	Ala	Gln	Asn	Ile
25			35					40					45			
	Ser	Leu 50	Ser	Glu	Leu	Val	Val 5'5	Phe	Trp	Gln	Asp	G1h	Gln \	Lys	Leu	Val
30	Leu	Tyr	Glu	His	Tyr		Gly	Thr	Glu	Lys	Leu	Asp	\ Şer	Val	Asn	Ala
30	65					70					75			•	,	80
	Lys	Tyr	Leu	Gly	Arg 85	Thr	Ser	Phe	Asp	Arg 90	Asn-	Asn	Trb	Thr	Leu 95	Arg
35	Leu	His	Asn	Val	Gln.	Ile	Lys	Asp		Gly	Ser	Tyr	Asp	Çys	Phe	Ile
				100					105					1/10		
, 40	Gln	Lys	Lys 115	Pro	Pro	Thr	Gly	Ser 120	Ile	Ile	Leu	Gln	Gln 125	The	Leu	Thr
/1,0	Glu	Leu	Ser	Val	Ile	Ala		Phe	Ser	Glu	Pro	Glu	Ile	Lys	Leu	Ala
		130					135			•		140				
45	Gln 145	Asn	Val	Thr	Gly	Asn 150	Ser	Gly	Ile	Asn	Leu 155	Thr	Cys	Thr	ser	Lys 160
	Gln	Gly	His	Pro	Lys 165	Pro	Lys	Lys	Met	Tyr 170	Phe	Leu	Ile	Thr	Asn 175	Ser
50	Thr	Asn	Glu	Tyr	Gly	Asp	Asn	Met	Gln	Ile	Ser	Gln	Asp	Asn	Val	Thr
-		•		180			. "		185		-		· F	190		
-	Glu	Leu	Phe	Ser	Ile	Ser	Asn	Ser	Leu	Ser.	Leu	Ser		Pro	Asp	GlX
55	•		195	-	-		•	200			•		205.		-	
	Val	Trp 210	His	Met	Thr	Val		Cys	Val	Leu	Glu		Glu	Ser	Met	Lys \
						•	215					220				. \

•	Ile Ser Ser Lys Pro Let Asn Phe Thr Gln Glu Phe Pro Ser Pro Gln 225 230 235 240	
5	Thr Tyr Trp Lys Glu Ile Thr Ala Ser Val Thr Val Ala Leu Leu Leu 245 250 255	
-	Val Met Leu Leu Ile Ile Val Cys His Lys Lys Pro Asn Gln Pro Ser 260 265 270	
10	Arg Pro Ser Asn Thr Ala Ser Lys Leu Glu Arg Asp Ser Asn Ala Asp 275 280 285	
15	Arg Glu Thr Ile Asn Leu Lys Glu Leu Glu Pro Gln Ile Ala Ser Ala 290 295 300	
13	Lys Pro Asn Ala Glu 305	
20	(2) INFORMATION FOR SEQ ID NO:22:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1120 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double	
25	(ii) MOLECULE TYPE: cDNA	
30	(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1071093	-
35 21	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:	
	CACAGGGTGA AAGCTTTGCT TCTCTGCTGC TGTAACAGGG ACTAGCACAG ACACACGGAT	60
40	GAGTGGGGTC ATTTCCAGAT ATTAGGTCAC AGCAGAAGCA GCCAAA ATG GAT CCC Met Asp Pro 1	115
45	CAG TGC ACT ATG GGA CTG AGT AAC ATT CTC TTT GTG ATG GCC TTC CTG Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu 5	163
50	CTC TCT GGT GCT GCT CTG AAG ATT CAA GCT TAT TTC AAT GAG ACT Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr 20 25 30 35	211
JU .	GCA GAC CTG CCA TGC CAA TTT GCA AAC TCT CAA AAC CAA AGC CTG AGT Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser 40 45 50	259
55	GAG CTA GTA GTA TTT TGG CAG GAC CAG GAA AAC TTG GTT CTG AAT GAG Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu 55	307





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-	GAT Asp	GAA	GCC Ala 310	Gln	CGT Arg	GTT Val	TTI Phe	AAA Lys 315	Ser	TCG Ser	AÅG Lys	ACA Thr	TCT Ser 320	Ser	TGC Cys	GAC Asp	
			Asp		TGT Cys			AATT.	AGA	GTAA	AGCC	CA A	AAAA	AA		: :	
10	(2)	INF	ORMA	TION	FOR	SEQ	ID	NO:2	3 ;								
•							•	ERIS'	- \	•							
15				- (A (B) LEI	NGTH PE:	: 32 amin	9 am o ac line	ino\ id		s						-
		. (ii)	MOLE	CULE	TYP	E: p	rote	in			•					
20		(:	xi)	SEQU	ENCE	DES	CRIP	TION	: SE	Q ID,	, ио : :	23:					
	Met 1	Asp	Pro	Gln	Cys 5	Thr	Met	Gly	Leu	Ser 10	Asn	Ile	Leu	Phe	Val 15	Met	
25	Ala	Phe	Leu	Leu 20	Ser	Gly	Ala	Ala	Pro 25	Leu	Lys	Ile	Gln	Ala 30	Tyr	Phe	
30	Asn	Glu	Thr 35	Ala	Asp	Leu	Pro	Cys 40	Gln	Phe	Ala	Asn	Ser 45	Gln	Asn	Gln	
	Ser	Leu 50	Ser	Glu	Leu	Val	Val 55	Phe	Trp	Gln	Asp	Gl'n	Glu	Asn	Leu	Val	
7 ³⁵	Leu 65	Asn	Glu	Val	Tyr	Leu 70	Gly	Lys	Glu	Lys	Phe 75	Asp	Ser	Val	His	Ser 80	-
	Lys	Tyr	Met	Gly	Arg 85	Thr	Ser	Phe	Asp	Ser 90	Asp	Ser	Trp,	Thr	Leu 95	Arg	
40	Leu	His	Asn	Leu 100	Gln	Ile	Lys	Asp	Lys 105	Gly	Leu	Tyr	Gln	Cys	Ile	Ile	
45	His	His	Lys 115	Lys	Pro	Thr	Gly	Met 120	Ile	Arg	Ile	His	Gln 125	Met'	Asn	Ser	
	Glu	Leu 130	Ser	Val	Leu	Ala	Asn 135	Phe	Ser	Gln	Pro	Glu 140	Ile	Val	Pro	Ile	
50	Ser 145	Asn	Ile	Thr	Glu	Asn 150	Val	Tyr	lle	Asn	Leu 155	Thr	Cys	Ser	Ser	Ile 160	
-	His	Gly	Tyr	Pro	Glu 165	Pro	Lys	Lys	Met	Ser 170	Val.	Leu	Leu	Arg	Thr 175	Lys	
55	Asn	Ser	Thr	Ile 180	Glu	Tyr	-Asp	Gly	Ile 185	Met	Gln	Lys	Ser	Gln 190	Asp	Asn	
	Val	Thr	Glu 195	Leu	Tyr	Asp	Val	Ser 200	Ile	Ser	Leu	Ser	Val 205	Ser	Phe	Pro	

	_											
	Asp Val Thr Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys 210 220											
5	Thr Arg Leu Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln 225 230 230 240											
10	Pro Pro Pro Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val 245 250 255											
	Ile Ile Cys Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys 260 270											
15	Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu 275 280 285											
	Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro 290 295 300											
20	Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser											
25	Ser Cys Asp Lys Ser Asp Thr Cys Phe 325											
	(2) INFORMATION FOR SEQ ID NO:24:											
30 (dy)	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 1161 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear											
35	(ii) MOLECULE TYPE: cDNA											
40	(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 1481134	-										
	(Xi) SEQUENCE DESCRIPTION, SEQ ID NO 24											
45	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24: AGGAGCCTTA GGAGGTACGG GGAGCTCGCA AATACTCCTT TTGGTTTATT CTTACCACCT											
	TGCTTCTGTG TTCCTTGGGA ATGCTGCTGT GCTTATGCAT CTGGTCTCTT TTTGGAGCTA	120										
	CAGTGGACAG GCATTTGTGA CAGCACT ATG GAT CCC CAG TGC ACT ATG GGA Met Asp Pro Gln Cys Thr Met Gly	171										
50	1 5	-										
55	CTG AGT AAC ATT CTC TTT GTG ATG GCC TTC CTG CTC TCT GGT GCT Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu Leu Ser Gly Ala Ala 10 15 20	219										
	CCT CTG AAG ATT CAA GCT TAT TTC AAT GAG ACT GCA GAC CTG CCA TGC Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr Ala Asp Leu Pro Cys 30 35 40	267										

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	CAA Gln	TTI Phe	GCA Ala	AAC Asn	TCT Ser 45	Glþ	AAC Asn	CAA Gln	AGC Ser	CTC Leu	ı Ser	GAC	CT?	A GT <i>I</i> 1 Va]	A GTA Val	TTT Phe	-	315
, 5	TGG Trp	CAG Gln	GAC Asp	CAG Gln 60	Glu	AAC Asn	TG	GTT Val	CTG Leu 65	Asn	GAG	GTA Val	TAC	TTA Leu	Gly	AAA Lys		363
10	GAG Glu	AAA Lys	TTT Phe 75	Asp	AGT Ser	GTT Val	CAT His	TCC Ser 80	AAG Lys	TAT	ATG Met	GGC Gly	CGC Arg	Thr	AGT Ser	TTT Phe		411
15	GAT A sp	TCG Ser 90	GAC Asp	AGT Ser	TGG Trp	ACC Thr	CTG Leu 95	AGA Arg	CTT Leu	CAC	AAT Asn	CTT Leu 100	Gln	ATC	AAG Lys	GAC Asp		459
20	AAG Lys 105	GGC	TTG Leu	TAT Tyr	CAA Gln	TGT Cys 110	ATC Ile	ATC Ile	CAT His	CAC His	AAA Lys 115	Lys	CCC	ACA Thr	GGA Gly	ATG Met 120		507
	Ile	Arg	ATC Ile	His	Gln 125	Met	Asn	Ser	Glu	Leu 130	Ser \	Val	Leu	Ala	Asn 135	Phe		555
25	Ser	Gln	CCT Pro	Glu 140	Ile	Val	Pro	Ile	Ser 145	Asn	Île	Thr	Glu	Asn 150	Val	Tyr		603
30	ATA Ile	AAT Asn	TTG Leu 155	ACC Thr	TGC Cys	TCA Ser	TCT Ser	ATA Ile 160	CAC His	GGT Gly	TAC	CCA Pro	GAA Glu 165	CCT Pro	AAG Lys	AAG Lys		651
35	ATG Met	AGT Ser 170	GTT Val	TTG Leu	CTA Leu	Arg	ACC Thr 175	AAG Lys	AAT Asn	TCA Ser	ACT Thr	ATC Ile 180	GAG \Glu	TAT Tyr	GAT Asp	GGT Gly		699
40	11e 185	Met	CAG Gln	Lys	Ser	Gln 190	Asp	Asn	Val	Thr	Glu 195	Leu	Tyż	Asp	Val	Ser 200		747
	He	Ser	TTG Leu	Ser	Val 205	Ser	Phe	Pro	Asp	Val 210	Thr	Ser	Asn	Met	Thr 215	Ile		795
45	Pne	Cys	ATT Ile	Leu 220	Glu	Thr .	Asp	Lys	Thr 225	Arg	Leu	Leu	Ser	Ser 230	Pro	Phe	i	843
50	ser	Ile	GAG Glu 235	Leu	Glu	Asp	Pro	Gln 240	Pro	Pro	Pro	Asp	His 245	Ile	Pro\	Trp		391 :
55		Thr 250	Ala	Val	Leu	Pro '	Thr 255	Val	Ile	Ile	Cys .	Val 260	Met	Val	Phe	Cys	-9	939-
	CTA . Leu 265	ATT Ile	CTA Leu	TGG . Trp	Lys	TGG 2 Trp 1 270	AAG . Lys :	AAG Lys	AAG Lys	Lys	CGG Arg 275	CCT Pro	CGC Arg	AAC Asn	TCT Ser	TAT\ Tyr 280	9	987



5	AAA TGT GGA ACC AAC ACA ATG GAG AGG GAA GAG AGT GAA CAG ACC AAG Lys Cys Gly Thr Asn Thr Met Glu Arg Glu Glu Ser Glu Gln Thr Lys 285 290 295	1035
·	AAA AGA GAA AAA ATC CAT ATA CCT GAA AGA TCT GAT GAA GCC CAG CGT Lys Arg Glu Lys Ile His Ile Pro Glu Arg Ser Asp Glu Ala Gln Arg 300 305 310	1083
10	GTT TTT AAA AGT TCG AAG ACA TCT TCA TGC GAC AAA AGT GAT ACA TGT Val Phe Lys Ser Ser Lys Thr Ser Ser Cys Asp Lys Ser Asp Thr Cys 315 320 325	1131
15	TTT TAATTAAAGA GTAAAGCCCA AAAAAAA Phe	1161
20	(2) INFORMATION FOR SEQ ID NO:25:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 629 base pairs (B) TYPE: nucleic acid	
25	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	,
30	(ix) FEATURE: (A) NAME/KEY: CDS	
7 h	(B) LOCATION: 196 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:	
, ,,	AGA AGC TGT TTC AGA AGA AAT GAG GCA AGC AGA GAA ACA AAC AAC AGC Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu Thr Ash Asn Ser	48
40	CTT ACC TTC GGG CCT GAA GAA GCA TTA GCT GAA CAG ACC GTC TTC GTT	0.5 :
	Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln Thr Val Phe Leu 20 25 30	96
45	TAGTTCTTCT CTGTCCATGT GGGATACATG GTATTATGTG GCTCATGAGG TACAATCTTT	156
	CTTTCAGCAC CGTGCTAGCT GATCTTTCGG ACAACTTGAC ACAAGATAGA GTTAACTGGG	216
50		276
		336
55		396
		456
		516
	GAGGGCCTGG GAGGAGAGA GGGAGGGGA CGGGGTGGGG GTGGGGAAAA CTATGGTTGG	576



	GATGTAAAAA CGGATAATAA TATAAATATT AAATAAAAAG AGAGTATTGA GCA	629
5	(2) INFORMATION FOR SEQ ID NO:26:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 32 amino acids (B) TYPE: amino acid (D) TOPOLOGY: linear	
10		
	(ii) MOLECULE TYPE: protein	
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:	
	Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser Arg Glu Thr Asn Asn Ser 1 5 10 15	
20	Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala Glu Gln Thr Val Phe Leu 20 25 30	
	(2) INFORMATION FOR SEQ ID NO:27:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 379 base pairs (B) TYPE: nucleic acid	
30 L	(C) STRANDEDNESS: double (D) TOPOLOGY: linear	
40	(ii) MOLECULE TYPE: cDNA	
35	(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 169	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:	
	TGC TTT GCC CCA AGA TGC AGA GAG AGA AGG AGG AAT GAG AGA TTG AGA Cys Phe Ala Pro Arg Cys Arg Glu Arg Arg Arg Asn Glu Arg Leu Arg 1 5 10 15	48
45	AGG GAA AGT GTA CGC CCT GTA TAACAGTGTC CGCAGAAGCA AGGGGCTGAA Arg Glu Ser Val Arg Pro Val 20	99
50	AAGATCTGAA GGTAGCCTCC GTCATCTCTT CTGGGATACA TGGATCGTGG GGATCATGAG	159
	GCATTCTTCC CTTAACAAAT TTAAGCTGTT TTACCCACTA CCTCACCTTC TTAAAAACCT	219
	CTTTCAGATT AAGCTGAACA GTTACAAGAT GGCTGGCATC CCTCTCCTTT CTCCCCATAT	279
55 -	GCAATTTGCT TAATGTAACC TCTTCTTTTG CCATGTTTCC ATTCTGCCAT CTTGAATTGT	339
	CTTGTCAGCC AATTCATTAT CTATTAAACA CTAATTTGAG	379

96

145

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(2)	INFORMATION	FOR	SEQ	ID	NO:28
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(i)	SECTIENCE	CHARACTERISTICS	
. – ,		CHANGERERISITES	2

- (A) LENGTH: 23 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: Ninear
- (ii) MOLECULE TYPE: protein
- 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Cys Phe Ala Pro Arg Cys Arg Glu\Arg Arg Arg Asn Glu Arg Leu Arg 10

- 15 Arg Glu Ser Val Arg Pro Val 20
 - (2) INFORMATION FOR SEQ ID NO:29:
- 20 (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 261 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

CAC AAG AAG CCG AAT CAG CCT AGC AGG CCC AGC AAC ACA GCC TCT AAG His Lys Lys Pro Asn Gln Pro Ser Arg Pro Ser Asn Thr Ala Ser Lys

TTA GAG CGG GAT AGT AAC GCT GAC AGA GAG ACT ATC AAC\CTG AAG GAA 40 Leu Glu Arg Asp Ser Asn Ala Asp Arg Glu Thr Ile Asn Leu Lys Glu

CTT GAA CCC CAA ATT GCT TCA GCA AAA CCA AAT GCA GAG TGAAGGCAGT Leu Glu Pro Gln Ile Ala Ser Ala Lys Pro Asn Ala Glu 45

GAGAGCCTGA GGAAAGAGTT AAAAATTGCT TTGCCTGAAA TAAGAAGTGC AGAGTTTCTC

50 AGAATTCAAA AATGTTCTCA GCTGATTGGA ATTCTACAGT TGAATAATTA AAGAAC 261

(2) INFORMATION FOR SEQ ID NO:30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 45 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

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(ii)	MOLECULE	TYPE:	proteir
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

His Lys Lys Pro Asn Gln Pro Ser Arg Pro Ser Asn Thr Ala Ser Lys 10

Leu Glu Arg Asp Ser Asn Ala Asp Arg Glu Thr Ile Asn Leu Lys Glu 25

Leu Glu Pro Gln Ile Ala Ser Ala Lys Pro Asn Ala Glu 40

(2) INFORMATION FOR SEQ ID NO:31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

25 (ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..183

30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

AAA TGG AAG AAG AAG CGG CCT CGC AAC TCT TAT AAA TGT GGA ACC 48 Lys Trp Lys Lys Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr

AAC ACA ATG GAG AGG GAA GAG AGT GAA CAG ACC AAG AAA AGA GAA AAA 96 Asn Thr Met Glu Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys 20

ATC CAT ATA CCT GAA AGA TCT GAT GAA GCC CAG CGT GTT TTT AAA AGT 40 144 Ile His Ile Pro Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser 35 40

TCG AAG ACA TCT TCA TGC GAC AAA AGT GAT ACA TGT TTT TAATTAAAGA 193 45 Ser Lys Thr Ser Ser Cys Asp Lys Ser Asp Thr Cys Phe 50

GTAAAGCCCA AAAAAA

210

(2) INFORMATION FOR SEQ ID NO:32:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: protein



(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Lys Trp Lys Lys Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr
1 5 10 15

Asn Thr Met Glu Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys
20 25 30

Ile His Ile Pro Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser

35 40 45

Ser Lys Thr Ser Ser Cys Asp Lys Ser Asp Thr Cys Phe
50 55 60

- 15 (2) INFORMATION FOR SEQ ID NO:33:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 359 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: double
 - (D) TOPOLOGY: linear
 - (ii) MOLECULE TYPE: cDNA

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- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 249..359

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

	GAGTTTTATA CCTCAATAGA CTCTTACTAG TTTCTCTTTT TCAGGTTGTG AAACTCAACC	60
35	TTCAAAGACA CTCTGTTCCA TTTCTGTGGA CTAATAGGAT CATCTTTAGC ATCTGCCGGG	120
	TGGATGCCAT CCAGGCTTCT TTTTCTACAT CTCTGTTTCT CGATTTTTGT GAGCCTAGGA	180
40	GGTGCCTAAG CTCCATTGGC TCTAGATTCC TGGCTTTCCC CATCATGTTC TCCAAAGCAT	240
	CTGAAGCT ATG GCT TGC AAT TGT CAG TTG ATG CAG GAT ACA CCA CTC CTC Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu 1 5 10	290
45	AAG TTT CCA TGT CCA AGG CTC AAT CTT CTC TTT GTG CTG CTG ATT CGT Lys Phe Pro Cys Pro Arg Leu Asn Leu Leu Phe Val Leu Leu Ile Arg 15 20 25 30	338
50	CTT TCA CAA GTG TCT TCA GAT	250

(2) INFORMATION FOR SEQ ID NO:34:

35

Leu Ser Gln Val Ser Ser Asp

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

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(iii	MOLECULE	TVDF.	nrotein
,		IIFC:	DIOLETII

(xi)	SEQUENCE	DESCRIPTION:	SEO	ID	NO - 34 -

Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe ્ 5

Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser 10 20 **25** . . 30

Gln Val Ser Ser Asp 35

15 (2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 416 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: cDNA

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(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 318..416

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

	CCAAAGAAAA AGTGATTTGT CATTGCTTTA TAGACTGTAA GAAGAGAACA TCTCAGAAGT	60
35	GGAGTCTTAC CCTGAAATCA AAGGATTTAA AGAAAAAGTG GAATTTTTCT TCAGCAAGCT	120
	GTGAAACTAA ATCCACAACC TTTGGAGACC CAGGAACACC CTCCAATCTC TGTGTGTTTT	180
40	GTAAACATCA CTGGAGGGTC TTCTACGTGA GCAATTGGAT TGTCATCAGC CCTGCCTGTT	240
	TTGCACCTGG GAAGTGCCCT GGTCTTACTT GGGTCCAAAT TGTTGGCTTT CACTTTTGAC	300
45	CCTAAGCATC TGAAGCC ATG GGC CAC ACA CGG AGG CAG GGA ACA TCA CCA Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro 1 5 10	350
50	TCC AAG TGT CCA TAC CTG AAT TTC TTT CAG CTC TTG GTG CTG GCT GGT Ser Lys Cys Pro Tyr Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly 15 20 25	398
	CTT TCT CAC TTC TGT TCA Leu Ser His Phe Cys Ser 30	416

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- (2) INFORMATION FOR SEQ ID NO:36:
 - (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 33 amino acids

	- 84 -	3/6
	(B) TYPE: amino acid (D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: protein	
3	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:	
10	Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser Lys Cys Pro Tyr 1 5 10 15	
	Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu Ser His Phe Cys 20 25 30	
15	Ser	
	(2) INFORMATION FOR SEQ ID NO:37:	
20	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 113 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
25	(ii) MOLECULE TYPE: cDNA	
30	(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 99113	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:	
35	GGAGCAAGCA GACGCGTAAG AGTGGCTCCT GTAGGCAGCA CGGACTTGAA CAACCAGACT	60
	CCTGTAGACG TGTTCCAGAA CTTACGGAAG CACCCACG ATG GAC CCC AGA TGC Met Asp Pro Arg Cys 1 5	113
40	• • • · · · · · · · · · · · · · · · ·	
	(2) INFORMATION FOR SEQ ID NO:38:	
45	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 5 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear	
-0	(ii) MOLECULE TYPE: protein	

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Met Asp Pro Arg Cys

50

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1 Sp Pro Arg Cys

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 124 base pairs

	(B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: cDNA	
10	(ix) FEATURE: (A) NAME/KEY: CDS (B) LOCATION: 107124	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:	
15	CACAGGGTGA AAGCTTTGCT TCTCTGCTGC TGTAACAGGG ACTAGCACAG ACACACGGAT	60
20	GAGTGGGGTC ATTTCCAGAT ATTAGGTCAC AGCAGAAGCA GCCAAA ATG GAT CCC Met Asp Pro 1	115
20	CAG TGC ACT Gln Cys Thr 5	124
25	(2) INFORMATION FOR SEQ ID NO:40:	
30	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 6 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: protein	
35	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:	
	Met Asp Pro Gln Cys Thr 1 5	
40	(2) INFORMATION FOR SEQ ID NO:41:	
45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 195 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: double (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
50		

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 148..195

55

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:



	TGCTTCTGTG TTCCTTGGGA ATGCTGCTGT GCTTATGCAT CTGGTCTCTT TTTGGAGCTA	120
5	CAGTGGACAG GCATTTGTGA CAGCACT ATG GGA CTG AGT AAC ATT CTC TTT Met Gly Leu Ser Asn Ile Leu Phe 1 5	171
10	GTG ATG GCC TTC CTG CTC TCT GGT Val Met Ala Phe Leu Leu Ser Gly 10 15	195
	(2) INFORMATION FOR SEQ ID NO:42:	
15	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 16 amino acids(B) TYPE: amino acid(D) TOPOLOGY: linear	
20	(ii) MOLECULE TYPE: protein	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:	
25	Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu Leu Ser Gly 1 5 10 15	
	(2) INFORMATION FOR SEQ ID NO: 43:	
30	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	
35	(D) TOPOLOGY: linear (ii) MOLECULE TYPE: oligonucleotide	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:	
40	CCAACATAAC TGAGTCTGGA AA	22 [.]
	(2) INFORMATION FOR SEQ ID NO: 44:	22
45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	,
50	(ii) MOLECULE TYPE: oligonucleotide	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:	
55	CTGGATTCTG ACTCACCTTC A	21
	(2) INFORMATION FOR SEQ ID NO: 45:	
	(i) SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 21 base pairs

	•	
	(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
5	(ii) MOLECULE TYPE: oligonucleotide	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:	
10	AGGTTAAGAG TGGTAGAGCC A	21
	(2) INFORMATION FOR SEQ ID NO: 46:	
15	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
20	(ii) MOLECULE TYPE: oligonucleotide	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:	
	AATACCATGT ATCCCACATG G	21
25	(2) INFORMATION FOR SEQ ID NO: 47:	
30	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: oligonucleotide	
35 ,	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:	
	CTGAAGCTAT GGCTTGCAAT T	21
40	(2) INFORMATION FOR SEQ ID NO: 48:	
45	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: oligonucleotide	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:	
50	TGGCTTCTCT TTCCTTACCT T	 21
	(2) INFORMATION FOR SEQ ID NO: 49:	
55	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	-

(D) TOPOLOGY: linear

	· ·	
	(ii) MOLECULE TYPE: oligonucleotide	
5	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:	
3	GCAAATGGTA GATGAGACTG T	. 21
	(2) INFORMATION FOR SEQ ID NO: 50:	
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs	
	(B) TYPE: nucleic adid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
15		
	(ii) MOLECULE TYPE: oligonucleotide	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:	
20	CAACCGAGAA ATCTACCAGT AA	22
	(2) INFORMATION FOR SEQ ID NO: 51:	
25	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: oligonucleotide	
•	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: \51:	
35	GCCGGTAACA AGTCTCTTCA	20
	(2) INFORMATION FOR SEQ ID NO: 52:	
40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
45	(ii) MOLECULE TYPE: oligonucleotide	
,,,	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:	
	AAAAGCTCTA TAGCATTCTG TC	22
50	(2) INFORMATION FOR SEQ ID NO: 53:	:
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs	
55	(B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: oligonucleotide	

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:	. :	
	ACTGACTTGG ACAGTTGTTC A		21
5	(2) INFORMATION FOR SEQ TD NO: 54:	N.	:
10	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear		×-
	(ii) MOLECULE TYPE: oligonucleotide		
15	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:		-
	TTTGATGGAC AACTTTACTA		20
20	(2) INFORMATION FOR SEQ ID NO: 55:	•	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single		
25	(D) TOPOLOGY: linear		
	(ii) MOLECULE TYPE: oligonucleotide		
30	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:		
	CAGCTCACTC AGGCTTATGT		20
	(2) INFORMATION FOR SEQ ID NO: 56:	um.	
35 20 40	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear		
.0	(ii) MOLECULE TYPE: oligonucleotide		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:		
45	AAACAGCATC TGAGATCAGC A		21
	(2) INFORMATION FOR SEQ ID NO: 57:		
50	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 		
55	(ii) MOLECULE TYPE: oligonucleotide		•
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:		
	CTGAGATCAG CAAGACTGTC		2.0

	WO 95/23859	PCT/US95/02576
	58 y - 90 -	,
	(2) INFORMATION FOR SEQ ID NO: 58:	•
5	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: oligonuoleotide	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58: CTGAAGCTAT GGCTTGCAAT T	21
15	(2) INFORMATION FOR SEQ ID NO: 59:	
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
25	(ii) MOLECULE TYPE: oligonucleotide	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:	
	ACAAGTGTCT TCAGATGTTG AT	22
30	(2) INFORMATION FOR SEQ ID NO: 60:	
かる	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: oligonucleotide	
40	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:	
	CTGGATTCTG ACTCACCTTC A	21
45	(2) INFORMATION FOR SEQ ID NO: 61:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid	
50	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: oligonucleotide	
55	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:	7.2
	CCAGGTGAAG TCCTCTGACA	20

(2) INFORMATION FOR SEQ ID NO:62:

		(i) S		NCE (LENG:					•	٠							
5				(B) (C)	TYPE STRAI	: nu	clei NESS	c ac : do	id uble									
		12							1				•				-	
10					ULE 7	PYPE	: cD	NA	\							•		
10		(i:			RE: NAME/ LOCAT				84									
15		(x:	i) sı	EQUE	NCE I	DESCI	RIPT	ON:	SEQ	ip 1	10:62	2:	-					
	GAG	TTT	ATA	CCT	CAATA	AGA C	CTCTI	TACT	AG TI	TCT	TTTT	TC	AGGT"	rgtg	AAA	CTCA	ACC	6
20	TTC	AAAC	ACA	CTCI	GTTC	CA 1	TTCI	rgrgo	SA CI	ATAA:	GGAI	CAT	CTT	TAGC	ATC	rgcco	GGG	12
	TGG	ATGO	CAT	CCAG	GCTI	CT I	TTTC	TAC	T CI	CTGI	TTCI	CGZ	TTT:	rtgt	GAG	CCTAC	G GA	18
	GGT	GCCI	AAG	CTCC	ATTG	GC I	CTAC	ATTO	C TG	GCTI	TCÇC	CAI	CATO	TTC	TCC	AAAGO	CAT	24
25	CTG	AAGC	T AT	G GC	T TG	C AA	T TG	T CA	G TI	G AI	G CA	G GA	T AC	ZA CO	CA CI	C CI	rc	29
知			Me	1	а Су	's As	n Cy	s Gl 5	n Le	u Me	t Gl		p Th	ır Pı	o Le	u Le	eu .	
30	AAG Lys 15	Phe	CCA Pro	TGT Cys	CCA Pro	AGG Arg 20	Leu	AAT Asn	CTT Leu	CTC	TTT Phe 25	vàl	CTG	CTC Lev	ATT	CGT Arg	ī	33
35	CTT Leu	TCA Ser	CAA Gln	GTG Val	TCT Ser 35	TCA Ser	GAT Asp	GTT Val	GAT Asp	GAA Glu 40	CAA Gln	CTG Leu	TCC	: AAG	TCA Ser 45	Val	;	386
40	AAA Lys	GAT Asp	AAG Lys	GTA Val 50	TTG Leu	CTG Leu	CCT Pro	TGC Cys	CGT Arg 55	TAC Tyr	AAC Asn	TCT Ser	CCT Pro	CAT His	Glu	GAT Asp	•	434
	GAG Glu	TCT Ser	GAA Glu 65	GAC Asp	CGA Arg	ATC Ile	TAC Tyr	TGG Trp 70	CAA Gln	AAA Lys	CAT His	GAC Asp	AAA Lys 75	.Val	GTG Val	CTG Leu		482
45	TCT Ser	GTC Val 80	ATT Ile	GCT Ala	GGG Gly	AAA Lys	CTA Leu 85	AAA Lys	GTG Val	TGG Trp	CCC Pro	GAG Glu 90	TAT Tyr	AAG	AAC Asn	CGG Arg		530
50	ACT Thr 95	TTA Leu	TAT Tyr	GAC Asp	AAC Asn	ACT Thr 100	ACC Thr	TAC Tyr	TCT Ser	CTT Leu	ATC Ile 105	ATC Ile	CTG Leu	GGC Gly	CTG Leu	GTC Val 110		578
55	CTT Leu	TCA Ser	GAC Asp	CGG Arg	GGC Gly 115	ACA Thr	TAC Tyr	AGC Ser	TGT Cys	GTC Val 120	GTT Val	CAA Gln	AAG Lys	AAG Lys	GAA Glu 125	AGA Arg		626
	GGA Gly	ACG Thr	TAT Tyr	GAA Glu 130	GTT Val	AAA Lys	CAC His	TTG Leu	GCT Ala 135	TTA Leu	GTA Val	AAG Lys	TTG Leu	TCC Ser 140	ATC Ile	AAA Lys		674

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	CCC CCA GAA GAC CCT CCT GAT AGC AAG AAC ACA CTT GTG CTC TTT GGG	722
	Pro Pro Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly	
5	150 155	
	GCA GGA TTC GGC GCA GTA ATA ACA GTC GTC GTC ATC GTC ATC ATC	
	Ala Gly Phe Gly Ala Val Ile The Val Val Val Ile Val Val Ile Ile	770
	160 165 170	
10		
10	AAA TGC TTC TGT AAG CAC AGA AGC TGT TTC AGA AGA AAT GAG GCA AGC	818
	Lys Cys Phe Cys Lys His Arg Ser Cys Phe Arg Arg Asn Glu Ala Ser	
	180 \ 185	
	AGA GAA ACA AAC AGC CTT ACC TTG GGG CCT GAA GAA GCA TTA GCT	866
15	Arg Glu Thr Asn Asn Ser Leu Thr Phe Gly Pro Glu Glu Ala Leu Ala	866
	195 200 205	
	Cha cha and and the things of the characters of	
	GAA CAG ACC GTC TTC CTT TAGTTCTTCT CTGTCCATGT GGGATACATG GTATTATGTG	924
20	210	
	GCTCATGAGG TACAATCTTT CTTTCAGCAC CGTGCTAGCT GATCTTTCGG ACAACTTGAC	984
	· · · · · · · · · · · · · · · · · · ·	
25	ACAAGATAGA GTTAACTGGG AAGAGAAAGC CTTGAATGAG GATTTCTTTC CATCAGGAAG	1044
	CTACGGGCAA GTTTGCTGGG CCTTTGATTG CTTGATGACT GAAGTGGAAA GGCTGAGCCC	
h	GAAGIGGAAA GGCTGAGCCC	1104
<i>با</i> ر	ACTGTGGGTG GTGCTAGCCC TGGGCAGGGG CAGGTGACCC TGGGTGGTAT AAGAAAAAGA	1164
۶.۱ 30	\	
50	GCTGTCACTA AAAGGAGAGG TGCCTAGTCT TACTGCAACT TGATATGTCA TGTTTGGTTG	1224
	GTGTCTGTGG GAGGCCTGCC CTTTTCTGAA GAGAAGTGGT GGGAGAGTGG ATGGGGTGGG	
	· \	1284
35	GGCAGAGGAA AAGTGGGGGA GAGGGCCCTGG GAGGAGAGGA	1344
22	GTGGGGAAAA CTATCCTTTCC CATGTAAAAA	
	GTGGGGAAAA CTATGGTTGG GATGTAAAAA CGGATAATAA TATAAATTT AAATAAAAAG	1404
	AGAGTATTGA GCA	1417
40		1417
40	(2) Typering	
	(2) INFORMATION FOR SEQ ID NO:63:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 212 amino acids	
45	(B) TYPE: amino acid	
	(D) TOPOLOGY: linear	
	(ii) NOT FIGURE TO THE	
	(ii) MOLECULE TYPE: protein	
50 -	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:	
-	Λ	
	Met Ala Cys Asn Cys Gln Leu Met Gln Asp Thr Pro Leu Leu Lys Phe	-
٠.	1 5 10 \ 15	
55	Pro Cvs Pro Arg Leu Tle Leu Lou Dhe vel Ten -	
	Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser	

Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp

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		-							1								
	Lys	Val 50	Leu	Leu	Pro	Cys	Arg 55	Tyr	Asn	Ser	Pro	His 60	Glu	Asp	Glu	Ser	
5	Glu 65	Asp	Arg	Ile	Tyr	Trp 70	Gln	Lys	His	Asp	Lys 75	Val	Val	Leu	Ser	Val	
10	Ile	Ala	Gly	Lys	Leu 85	Lys	Val	Trp	Pro	Glu 90	Tyr	Lys	Asn	Arg	Thr 95	Leu	•
	Tyr	Asp	Asn	Thr	Thr	Tyr	Ser	Leu	Ile 105	Ite	Leu	Gly	Leu	Val 110	Leu	Ser	
15	Asp	Arg	Gly 115	Thr	Tyr	Ser	Cys	Val 120	Val	Gln	Lys	Lys	Glu 125	Arg	Gly	Thr	
	Tyr	Glu 130	Val	Lys	His	Leu	Ala 135	Leu	Val	Lys	Leu	Ser 140	Ile	Lys	Pro	Pro	
20	Glu 145	Asp	Pro	Pro	Asp	Ser 150	Lys	Asn	Thr	Leu	Va 1 155	Leu	Phe	Gly	Ala	Gly 160	
25	Phe	Gly	Ala	Val	Ile 165	Thr	Val	Val	Val	Ile 170	Val	Val	Ile	Ile	Lys 175	Cys	
	Phe	Cys	Lys	His 180	Arg	Ser	Cys	Phe	Arg 185	Arg	Asn	Glu	Ala	Ser 190	Arg	Glu	
30	Thr	Asn	Asn 195	Ser	Leu	Thr	Phe	Gly 200	Pro	Glu	Glu	Ala	Leu 205	Ala	Glu	Gln	
	Thr	Val 210	Phe	Leu													
35	(2)	INFO	RMAT	'ION	FOR	SEQ	ID N	0:64	:			\					
40		(i)	(A (B (C	UENC) LE) TY) ST) TO	NGTH PE : RAND	: 16 nucl EDNE	06 b eic SS:	ase acid doub	pair	s		,					
45				ECUL		PE:	CDNA						\		٠		
		(1X)	(A	TURE) NAI) LO	ME/K								/	\			
50											-			1.			
								-		D NO	٠						
	GAG I"	ı T.I.Y.	TA C	CTCA	ATAG	A CT	CTTA(CTAG -	TTT	CTCT:	rtt :	rcago	GTTG:	rg ai	AACT	CAACC	6
55	TTCA	AAGA	CA C	TCTG'	TTCC	A TT	rctg:	TGGA	CTA	ATAGO	AT (CATC	TTA	3C A:	rctg	CCGGG	12
	TGGAT	rgcc.	AT C	CAGG	CTTC	r tr	TTCT	ACAT	CTC	rgtti	CT (CGAT	rttt	st di	AGCC	ragga	. 18
	GGTGC	CTA	AG C'	TCCA:	TTGG	C TC	raga:	TTCC	TGG	CTTTC	ccc c	CATC	ATGTT	C T	CAA	AGCAT	24

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	CT	GAAG	CT A	TG G(et A	CT TO	GC AI YS As	AT TO	GT CA YS G	AG T	TG A'	IG C	ln A	sp T	CA C	CA C	TC CT eu Le	c ·	290
5				_				_	- 1				10					
. •	AA(Ly: 1!	s Pn	T CC	A TGT	CC#	A AGG Arg 20	Let	AAT 1 Asi	r CT	r CTC	TT 1 Pho	e Va	G CT	G CT u Le	G AT	T CGT e Arg 30		338
10	CT: Let	r TC	A CAM	A GTO	G TCT Ser 35	Ser	GAI Asp	GTT Val	GAT Asi	GAZ Glu	A CAI 1 Gl:	A CTO	G TC	C AA	G TC: s Se: 4!	A GTG r Val 5		386
15	AA <i>I</i> Lys	A GAT	T AAG	GTA Val 50	ьeu	CTG Leu	CCT Pro	TGC Cys	CGT Arg	Тух	AAC	TC:	CC.	CA: Hi:	s Glu	A GAT		434
20	GAG Glu	TC1	GAA Glu	ı Asp	CGA Arg	ATC	TAC	TGG Trp 70	Gln	AAA Lys	CAT His	GAC Asp	C AAA Lys 75	Val	G GTO	G CTG L Leu		482
25	ser	80) . IIe	: Ala	GIA	Lys	Leu 85	Lys	Val	Trp	Pro	Ġlu ∕90 /	Туг	Lys	Asn	C CGG Arg		530
	95	Leu	ıyr	Asp	Asn	Thr 100	Thr	Tyr	Ser	Leu	Ile 105	Ilė	Leu	Gly	Leu	GTC Val 110		578
b ³⁰	CTT Leu	TCA Ser	GAC Asp	CGG Arg	GGC Gly 115	ACA Thr	TAC Tyr	AGC Ser	TGT Cys	GTC Val 120	GTT Val	CAA Gln	AAG Lys	AAG Lys	GAA Glu 125	_		626
35	GGA Gly	ACG Thr	TAT Tyr	GAA Glu 130	GTT Val	AAA Lys	CAC His	TTG Leu	GCT Ala 135	TTA Leu	GTA Val	ÀÀG Lys	TTG Leu	TCC Ser	Ile	AAA Lys		674
40	CCC Pro	CCA Pro	GAA Glu 145	GAC Asp	CCT Pro	CCT Pro	GAT Asp	AGC Ser 150	AAG Lys	AAC Asn	ACA Thr	CTT Leu	GTG Val 155	CTC	TTT Phe	GGG Gly		722
45	GCA Ala	GGA Gly 160	TTC Phe	GGC Gly	GCA Ala	GTA Val	ATA Ile 165	ACA Thr	GTC Val	GTC Val	GTC Val	ATC Ile 170	GTT Val	GTC Val	ATC Ile	ATC Ile		770
	AAA Lys 175	TGC Cys	TTC Phe	TGT Cys	AAG Lys	CAC His 180	GGT Gly	CTC Leu	ATC Ile	TAC Tyr	CAT His 185	TTG Leu	CAA Gln	CTG Leu	ACC Thr	TCT Ser 190	8	318
50	TCT	GCA Ala	AAG Lys	GAC Aşp	TTC Phe 195	AGA Arg	AAC Asn	CTA Leu	GCA Ala	CTA Leu 200	CCC Pro	TGG Trp	CTC Leu	TGC Cys	AAA Lys 205	CAC His	8	366 ,
55	GGT Gly	TCT Ser	CTA Leu	GGT Gly 210	GAA Glu	GCC Ala	TCT Ser	Ala	GTG Val 215	ATT Ile	TGC Cys	AGA Arg	AGT Ser	ACT Thr 220	CAG Gln	ACG Thr	- 9	914

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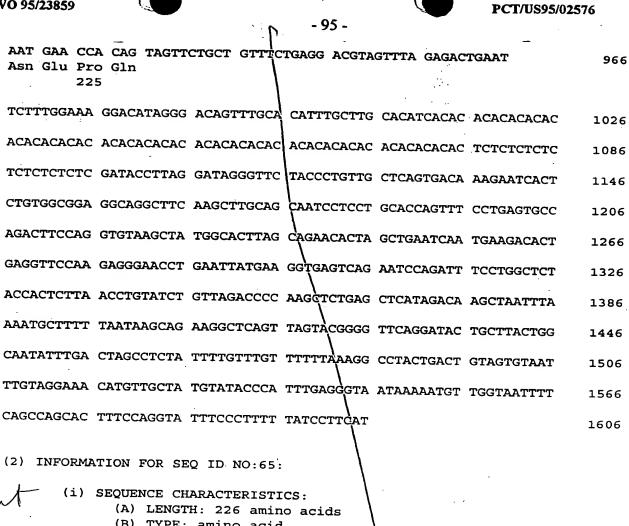
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- (B) TYPE: amino acid
- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

40	Met	Ala	Cys	Asn	Cys	${\tt Gln}$	Leu	Met	Gln	Asp	Thr	Pro	\ _{Leu}	Leu	Lvs	Phe
40	1			٠	5					10	•		[15	

Pro Cys Pro Arg Leu Ile Leu Leu Phe Val Leu Leu Ile Arg Leu Ser 30

Gln Val Ser Ser Asp Val Asp Glu Gln Leu Ser Lys Ser Val Lys Asp 45

Lys Val Leu Leu Pro Cys Arg Tyr Asn Ser Pro His Glu Asp Glu Ser 50

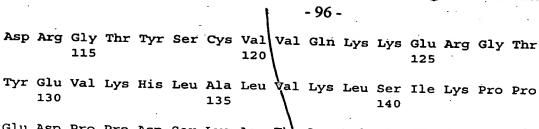
Glu Asp Arg Ile Tyr Trp Gln Lys His Asp Lys Val Val Leu Ser Val 75

Ile Ala Gly Lys Leu Lys Val Trp Pro Glu Tyr Lys Asn Arg Thr Leu 55 85

Tyr Asp Asn Thr Thr Tyr Ser Leu Ile Ile Leu Gly Leu Val Leu Ser 100

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Glu Asp Pro Pro Asp Ser Lys Asn Thr Leu Val Leu Phe Gly Ala Gly
150 155 160

10 Phe Gly Ala Val Ile Thr Val Val Val Val Val Ile Ile Lys Cys 165 170 175

Phe Cys Lys His Gly Leu Ile Tyr His Leu Gln Leu Thr Ser Ser Ala 180 185 190

Lys Asp Phe Arg Asn Leu Ala Leu Pro Trp Leu Cys Lys His Gly Ser
195 200 205

Leu Gly Glu Ala Ser Ala Val Ile Cys Arg Ser Thr Gln Thr Asn Glu 210 215 220

Pro Gln 225